

Sequence Listing

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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				110					115					120					
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu					
				125					130					135					
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly					
				140					145					150					
Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser					
				155					160					165					
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu					
				170					175					180					
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu					
				185					190					195					
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu					
				200					205					210					
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly					
				215					220					225					
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe					
				230					235					240					
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg					
				245					250					255					
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser					
				260					265					270					
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val					
				275					280					285					
Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr					
				290					295					300					
Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr					
				305					310					315					
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val					
				320					325					330					
Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr					
				335					340					345					

Pro	Asn	Val	Ser	Glu	Lys	Ile	Leu	Ile	Asp	Ile	Ile	Gly	Val	Asp
				350					355					360
Phe	Ala	Phe	Ala	Glu	Leu	Cys	Val	Val	Pro	Leu	Arg	Ile	Phe	Ser
				365					370					375
Phe	Phe	Pro	Val	Pro	Val	Thr	Val	Arg	Ala	His	Leu	Thr	Gly	Trp
				380					385					390
Leu	Met	Thr	Leu	Lys	Lys	Thr	Phe	Val	Leu	Ala	Pro	Ser	Ser	Val
				395					400					405
Leu	Arg	Ile	Ile	Val	Leu	Ile	Ala	Ser	Leu	Val	Val	Leu	Pro	Tyr
				410					415					420
Leu	Gly	Val	His	Gly	Ala	Thr	Leu	Gly	Val	Gly	Ser	Leu	Leu	Ala
				425					430					435
Gly	Phe	Val	Gly	Glu	Ser	Thr	Met	Val	Ala	Ile	Ala	Ala	Cys	Tyr
				440					445					450
Val	Tyr	Arg	Lys	Gln	Lys	Lys	Lys	Met	Glu	Asn	Glu	Ser	Ala	Thr
				455					460					465
Glu	Gly	Glu	Asp	Ser	Ala	Met	Thr	Asp	Met	Pro	Pro	Thr	Glu	Glu
				470					475					480
Val	Thr	Asp	Ile	Val	Glu	Met	Arg	Glu	Glu	Asn	Glu			
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<210> 8

<211> 535

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 66, 96, 387

<223> unknown base

<400> 8

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cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
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aagaataacc ccagcaacaa actgggtgagc acgagcaaca cagtcacggc 300
ggccacatc aagaagtcca cttcgtctg catggctctg tcaactcacgc 350
tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400
gacatcatcg gagggtgactt tgcctttgca gaactctgtg ttgttccttt 450

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gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500

ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc ccgggtggg tctctgggt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaacacagn acgggcagcc cacatcaaga 100

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gttttgga caaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgnngtg ttcctttgcg gattttctcc 250

tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcttac cctacctggg ggtgcacggt 400

gcgacctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

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acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100

cgctctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt.tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgccca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
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gcctgcctgg gagcctgtc cctgtcagc tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcactctgt gcagctgtg ccccgccagc cgcaactcca 150
ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgaggag agtcagctct acaagctgcc 250
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 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
 cagggctgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400
 aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctcc 1450
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 tggtcacgtc ccccagggga ccctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro
				20					25					30

Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
				35					40					45

Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
				50					55					60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu		
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
	455				

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 20
 gccgcctcat cttcacgttc ttcc 24

<210> 21
 <211> 20
 <212> DNA
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<220>
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<400> 21
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<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 22
 cttctttccac ttctgctgg 20

<210> 23
 <211> 18

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 23
 cctgggcaaa aatgcaac 18

 <210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 24
 caggaatgta gaaggcacc acgg 24

 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 25
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 <210> 26
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 26
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 <210> 27
 <211> 1351
 <212> DNA
 <213> Homo sapiens

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 ttaacctggg tcaaatgcac ggattctcac ctctgtacagt tacgctctcc 100
 cgcggcacgt ccgcgaggac ttgaagtcc gagcgtcaa gtttgtccgt 150
 aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
 tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
 cccagagccc tattaccgg aatctggatg ggaccgcctc cgggagctgt 350
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 aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
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 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
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t 1351

<210> 28
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
 20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
 ttcgttcatg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 262, 330, 371
 <223> unknown base

<400> 30
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 gcctccggga gctgtttggc aaagatgaac agcagagaaat ttcaaaggac 250
 cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
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 agagccaggc agaaatttat nataacc 377

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 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 31
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<210> 32
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<220>
 <223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
gctaataatct gtaagacggc agctacagca ggcattcattg 40

<210> 35
<211> 1819
<212> DNA
<213> Homo sapiens

<400> 35
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gacaaagcag ctgtcaggga acctcgcgcg gagtcgaatt tacgtgcagc 150
tgccggcaac cacagggtcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgcct caacctgctt tacaccttg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttcagtc 300
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gctttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttgatt tattgttcag tttctgtat 450
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550
aaactgctgt gggttccgaa gtgttaaccc aatgacacc tgtctggcta 600
gctgtgttaa aagtaccac tcgtgctgc catgtgctcc aatcatagga 650
gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
agaaagaccc ccgcgcgaat cctagtgc at tccctttgatg agaaaacaag 800
gaagatttcc ttctgtatta tgatcttggt cactttctgt aattttctgt 850
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atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
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taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo. sapiens

<400> 36

Met	Val	Cys	Gly	Gly	Phe	Ala	Cys	Ser	Lys	Asn	Cys	Leu	Cys	Ala
1				5					10				15	
Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25				30	

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	35	40	45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	50	55	60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	65	70	75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	80	85	90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	95	100	105
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	110	115	120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	125	130	135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	140	145	150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	155	160	165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	170	175	180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	185	190	195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							200		

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggtggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttgttgg tggcattggc ctgttnttca gttttacaga 350

gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

aatcccaa at tccccaat ttttggnc tttaggga gatgtgtgt 50

ggtaaaaagt gttagtataa aaatgataa ttactttag tcttttatga 100

ttacaccaat gtattctaga atagttagt cttaggaaat tgtggttta 150

tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200

tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250

ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300

taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgag 350

ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400

ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450

gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500

ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550

gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttggttagc ccctgaaacc aggagcaaca ggggncagct tcctggaggt 100

tggttgga caatcacggc caagtgactc cgcaaatgac atcccagaga 150

aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggtngctg tggtaaaagt gaccactcgt gctcgccatg tgcaccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

acccacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggcccaaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcaccat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150
cggaggatga cttgactgat gcaaggggaag ctggcttoca ggtcaaggcc 200
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350
gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400
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tgcagaggtc agctgcccgc ctctcttct ccttctacaa ggatggaagg 650
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 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
 20 25 30
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 tttccagcgc caattctc 18

 <210> 48
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 48
 agttcttgga ctgtgatagc cac 23

 <210> 49
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 49
 aaacttggtt gtcctcagtg gctg 24

 <210> 50
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 50
 gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

 <210> 51
 <211> 2181
 <212> DNA
 <213> Homo sapiens

 <400> 51
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 ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
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 gcacctaaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
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 tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggg 650
 ataagcaaca gactaataac caggaaccca tcaaagtagc aaccctaagt 700
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750
 cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800
 ttgtgggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850
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 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150
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 agggtcagga catagctgcc ttccctctct caggcacctt ctgagggtgt 1250
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 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
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 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr
 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180

Gln Thr Asn Asn	Gln Glu Pro Ile Lys	Val Ala Thr Leu Ser Thr	185	190	195
Leu Leu Phe Lys	Pro Ala Val Ile Ala Asp	Ser Gly Ser Tyr Phe	200	205	210
Cys Thr Ala Lys	Gly Gln Val Gly Ser Glu	Gln His Ser Asp Ile	215	220	225
Val Lys Phe Val	Val Lys Asp Ser Ser Lys	Leu Leu Lys Thr Lys	230	235	240
Thr Glu Ala Pro	Thr Thr Met Thr Tyr Pro	Leu Lys Ala Thr Ser	245	250	255
Thr Val Lys Gln	Ser Trp Asp Trp Thr Thr	Asp Met Asp Gly Tyr	260	265	270
Leu Gly Glu Thr	Ser Ala Gly Pro Gly Lys	Ser Leu Pro Val Phe	275	280	285
Ala Ile Ile Leu	Ile Ile Ser Leu Cys Cys	Met Val Val Phe Thr	290	295	300
Met Ala Tyr Ile	Met Leu Cys Arg Lys Thr	Ser Gln Gln Glu His	305	310	315
Val Tyr Glu Ala	Ala Arg		320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgccgggag cccatctgcc cccaggggca cggggcgcg ggcgggtcc 50

cgcccgccac atggctgcag ccacctcgcg cgcaccccga ggcgcccgc 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaacctg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaa aagtggatgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttctctg caggagatgc ctcccttcag attgaacctc tgaagcccag 500

tgatgagggc cggtaacact gtaagggttaa gaattcaggg cgctacgtgt 550

ggagccatgt catcttaaaa gtcttagtga gaccatccaa gccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

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 <212> PRT
 <213> Homo sapiens

<400> 59
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 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
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 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
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 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
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 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
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 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
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Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
Ser	Met	Ile	Pro	Ser	Gln	Ser	Arg	Ala	Phe	Gln	Thr	Val			365	370	

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<223> Synthetic oligonucleotide probe

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 61
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<210> 62
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<210> 63
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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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				20					25					30

Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	290	295	300
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	305	310	315
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly			

320	325	330
Pro Lys Arg Gly His 335	Pro Arg Gln Asn Leu His Lys His Phe 340	Asp 345
Ile Asn Glu His Leu 350	Pro Trp Met Ile Val Leu Phe Leu Leu 355	Leu 360
Val Leu Val Val Ile 365	Val Val Cys Ser Ile Arg Lys Ser Ser 370	Arg 375
Thr Leu Lys Lys Gly 380	Pro Arg Gln Asp Pro Ser Ala Ile Val 385	Glu 390
Lys Ala Gly Leu Lys 395	Lys Ser Met Thr Pro Thr Gln Asn Arg 400	Glu 405
Lys Trp Ile Tyr Tyr 410	Cys Asn Gly His Gly Ile Asp Ile Leu 415	Lys 420
Leu Val Ala Ala Gln 425	Val Gly Ser Gln Trp Lys Asp Ile Tyr 430	Gln 435
Phe Leu Cys Asn Ala 440	Ser Glu Arg Glu Val Ala Ala Phe Ser 445	Asn 450
Gly Tyr Thr Ala Asp 455	His Glu Arg Ala Tyr Ala Ala Leu Gln 460	His 465
Trp Thr Ile Arg Gly 470	Pro Glu Ala Ser Leu Ala Gln Leu Ile 475	Ser 480
Ala Leu Arg Gln His 485	Arg Arg Asn Asp Val Val Glu Lys Ile 490	Arg 495
Gly Leu Met Glu Asp 500	Thr Thr Gln Leu Glu Thr Asp Lys Leu 505	Ala 510
Leu Pro Met Ser Pro 515	Ser Pro Leu Ser Pro Ser Pro Ile Pro 520	Ser 525
Pro Asn Ala Lys Leu 530	Glu Asn Ser Ala Leu Leu Thr Val Glu 535	Pro 540
Ser Pro Gln Asp Lys 545	Asn Lys Gly Phe Phe Val Asp Glu Ser 550	Glu 555
Pro Leu Leu Arg Cys 560	Asp Ser Thr Ser Ser Gly Ser Ser Ala 565	Leu 570
Ser Arg Asn Gly Ser 575	Phe Ile Thr Lys Glu Lys Lys Asp Thr 580	Val 585
Leu Arg Gln Val Arg 590	Leu Asp Pro Cys Asp Leu Gln Pro Ile 595	Phe 600
Asp Asp Met Leu His 605	Phe Leu Asn Pro Glu Glu Leu Arg Val 610	Ile 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu
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635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

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<210> 67

<211> 50

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<400> 67

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<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 69
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 35 40 45
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 50 55 60
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly
 65 70 75
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala
 80 85 90
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr
 95 100 105
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

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His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr			
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Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe			
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Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys			
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Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala			
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Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg			
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Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu			
				215					220					225			
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His			
				230					235					240			
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala			
				245					250					255			
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile			
				260					265					270			
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His			
				275					280					285			
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg			
				290					295					300			
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr			
				305					310					315			
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu			
				320					325					330			
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala			
				335					340					345			
Thr	Glu	Asp	Gly	Gly	Asp	Ala	Ser	Pro	Val	Leu	Asn	His	Ala	Ala			
				350					355					360			
Val	Pro	Leu	Ile	Ser	Asn	Lys	Ile	Cys	Asn	His	Arg	Asp	Val	Tyr			
				365					370					375			
Gly	Gly	Ile	Ile	Ser	Pro	Ser	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Thr			
				380					385					390			
Gly	Gly	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val			
				395					400					405			

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe
 410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg
 425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp
 440 445 450

Leu Lys Thr

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgac cagcctgtgt gcctgcccac ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

cccacgcgtc cgtcctagtc cccggggccaa ctccggacagt ttgctcattt 50

attgcaacgg tcaaggctgg cttgtgccag aacggcgcg cgcgcgcac 100

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 <211> 735
 <212> PRT
 <213> Homo sapiens

<400> 74
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 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala
 35 40 45
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp
 50 55 60
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu
 65 70 75
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile
 80 85 90
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp
 95 100 105
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly
 110 115 120
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys
 125 130 135
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val
 140 145 150
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro
 155 160 165
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His
 170 175 180
 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser
 185 190 195
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr
 200 205 210

Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe Gln
215		220 225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile Glu
230		235 240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile Arg
245		250 255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys Cys
260		265 270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu Asp
275		280 285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn Ala
290		295 300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly Met
305		310 315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly Ile
320		325 330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr Leu
335		340 345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr Leu
350		355 360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly Cys
365		370 375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe Ser
380		385 390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly Met
395		400 405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe Gly
410		415 420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu Cys
425		430 435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn Ala
440		445 450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly Leu
455		460 465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys Arg
470		475 480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly Ala
485		490 495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His Ser

500					505					510				
Cys	Gln	Asp	Val	Asp	Gly	Tyr	Cys	Tyr	Asn	Gly	Ile	Cys	Gln	Thr
				515					520					525
His	Glu	Gln	Gln	Cys	Val	Thr	Leu	Trp	Gly	Pro	Gly	Ala	Lys	Pro
				530					535					540
Ala	Pro	Gly	Ile	Cys	Phe	Glu	Arg	Val	Asn	Ser	Ala	Gly	Asp	Pro
				545					550					555
Tyr	Gly	Asn	Cys	Gly	Lys	Val	Ser	Lys	Ser	Ser	Phe	Ala	Lys	Cys
				560					565					570
Glu	Met	Arg	Asp	Ala	Lys	Cys	Gly	Lys	Ile	Gln	Cys	Gln	Gly	Gly
				575					580					585
Ala	Ser	Arg	Pro	Val	Ile	Gly	Thr	Asn	Ala	Val	Ser	Ile	Glu	Thr
				590					595					600
Asn	Ile	Pro	Leu	Gln	Gln	Gly	Gly	Arg	Ile	Leu	Cys	Arg	Gly	Thr
				605					610					615
His	Val	Tyr	Leu	Gly	Asp	Asp	Met	Pro	Asp	Pro	Gly	Leu	Val	Leu
				620					625					630
Ala	Gly	Thr	Lys	Cys	Ala	Asp	Gly	Lys	Ile	Cys	Leu	Asn	Arg	Gln
				635					640					645
Cys	Gln	Asn	Ile	Ser	Val	Phe	Gly	Val	His	Glu	Cys	Ala	Met	Gln
				650					655					660
Cys	His	Gly	Arg	Gly	Val	Cys	Asn	Asn	Arg	Lys	Asn	Cys	His	Cys
				665					670					675
Glu	Ala	His	Trp	Ala	Pro	Pro	Phe	Cys	Asp	Lys	Phe	Gly	Phe	Gly
				680					685					690
Gly	Ser	Thr	Asp	Ser	Gly	Pro	Ile	Arg	Gln	Ala	Glu	Ala	Arg	Gln
				695					700					705
Glu	Ala	Ala	Glu	Ser	Asn	Arg	Glu	Arg	Gly	Gln	Gly	Gln	Glu	Pro
				710					715					720
Val	Gly	Ser	Gln	Glu	His	Ala	Ser	Thr	Ala	Ser	Leu	Thr	Leu	Ile
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<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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 ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150
 ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200
 gtagcagggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250
 aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300
 agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350
 gcagccctga taactggtnt ntggctgcaa nntaatgctn tgatattggc 400
 tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450
 gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctcagg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 77

catgagcatg tgcacggc 18

<210> 78

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 78

tacctgcacg atgggcac 18

<210> 79

<211> 18

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<213> Artificial Sequence

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 <400> 79
 cactgggcac ctcccttc 18

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 <223> Synthetic oligonucleotide probe

 <400> 80
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 <210> 81
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 <400> 81
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 <210> 82
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 cttcgctggg aagagtttg 19

 <210> 83
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 <400> 83
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 <210> 84
 <211> 1714
 <212> DNA
 <213> Homo sapiens

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<211> 67
<212> PRT
<213> Homo sapiens

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20 25 30
Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
35 40 45
Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
50 55 60
Ala Leu Leu His Leu Tyr His
65

<210> 86
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<220>
<223> Synthetic oligonucleotide probe

<400> 86
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<210> 87
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<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaagggca agcaagacc 29

<210> 88
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<220>

<223> Synthetic oligonucleotide probe

<400> 88

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<210> 89

<211> 2956

<212> DNA

<213> Homo sapiens

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gctgctgctg ggccatggcg gcggcgggcg ctggggcgcc cgggcccagg 150

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ggacaggacc cgcacagcaa gcacctgtac acggccgaca tgttcacgca 250

cgggatccag agcgcgcgcg acttcgtcat gttcttcgcg ccctgggtgtg 300

gacactgccg gcggctgcag ccgacttgga atgacctggg agacaaatac 350

aacagcatgg aagatgccaa agtctatgtg gctaaagtgg actgcacggc 400

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ggtggatcag tacaaggga agcgggattt ggagtcactg agggagtacg 900

tggagtgcga gctgcagcgc acagagactg gagcgacgga gaccgtcacg 950

ccctcagagg ccccggtgct ggcagctgag cccgaggctg acaagggcac 1000

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 tgtgttggtc cgtagcatgg agcagattga aatgcaaaaa cccacacctc 1850
 tggaagatac cttcacggcc gctgctggag cttctgttgc tgtgaatact 1900
 tctctcagtg tgagaggtta gccgtgatga aagcagcgtt acttctgacc 1950
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 tggatgtctt ccttagaaaag ggtaggcatg gaaaattcca cgaggctcat 2150
 tctcagtatc tcattaactc attgaaagat tccagttgta tttgtcacct 2200
 ggggtgacaa gaccagacag gctttcccag gcctgggtat ccaggagggc 2250
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 acctctatct cccttgggaa taagcacata caggcttaag ctctaagata 2550
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tgcattcaac actcttcacc cacctcccat acgcaagggg atgtggatac 2650
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 ctgtctgtct gaggcagaag ataacagcag catctcgacc agcctctgcc 2750
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 taaaaaaacc caacctccta gagaagcaca actgtcaaga gtcttgtaca 2850
 cacaacttca gctttgcac acgagtcttg tattccaaga aaatcaaagt 2900
 ggtacaattt gtttgtttac actatgatac tttctaaata aactcttttt 2950
 ttttaa 2956

<210> 90
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 90
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 20 25 30
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala
 35 40 45
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro
 50 55 60
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile
 65 70 75
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly
 80 85 90
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys
 95 100 105
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp
 110 115 120
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly
 125 130 135
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys
 140 145 150
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu
 155 160 165
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
 170 175 180

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91
 atgttcttcg cgccctggtg 20

<210> 92
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 92
 ccaagccaac acactctaca g 21

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 93
 aagtggtcgc cttgtgcaac gtgc 24

<210> 94
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 94
 ggtcaaaggg gatatatcgc cac 23

<210> 95
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 95
 gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggcca 49

<210> 96
 <211> 1016
 <212> DNA
 <213> Homo sapiens

<400> 96
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 aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100
 gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200
 agaggggaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaag 250
 gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300
 attgggaaga aggggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350
 agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400
 ttgttggaaca actggatatt agtattgctc ggctcaagac atctatgaag 450
 tttgtcaaga atgtgatagc agggattagg gaaactgaag agaaattcta 500
 ctacatcgtg caggaagaga agaactacag ggaatcccta acccactgca 550
 ggattcgggg tggaatgcta gccatgcca aggatgaagc tgccaacaca 600
 ctcacgctg actatgttgc caagagtggc ttctttcggg tggttcattgg 650
 cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700
 cactgcagaa ctatagcaac tggaatgagg gggaaccag cgaccctat 750
 ggtcatgagg actgtgtgga gatgctgagc tctggcagat ggaatgacac 800
 agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850
 agtaacttcc ctcacacctac gtatttgcta ttttcctgtg accgtcatta 900
 cagttattgt tatccatcct ttttttctg attgtactac atttgatctg 950
 agtcaacata gctagaaaat gctaaactga ggtatggagc ctccatcatc 1000
 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
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 Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

80					85					90				
Thr	Gly	Pro	Ile	Gly	Lys	Lys	Gly	Asp	Lys	Gly	Glu	Lys	Gly	Leu
				95					100					105
Leu	Gly	Ile	Pro	Gly	Glu	Lys	Gly	Lys	Ala	Gly	Thr	Val	Cys	Asp
				110					115					120
Cys	Gly	Arg	Tyr	Arg	Lys	Phe	Val	Gly	Gln	Leu	Asp	Ile	Ser	Ile
				125					130					135
Ala	Arg	Leu	Lys	Thr	Ser	Met	Lys	Phe	Val	Lys	Asn	Val	Ile	Ala
				140					145					150
Gly	Ile	Arg	Glu	Thr	Glu	Glu	Lys	Phe	Tyr	Tyr	Ile	Val	Gln	Glu
				155					160					165
Glu	Lys	Asn	Tyr	Arg	Glu	Ser	Leu	Thr	His	Cys	Arg	Ile	Arg	Gly
				170					175					180
Gly	Met	Leu	Ala	Met	Pro	Lys	Asp	Glu	Ala	Ala	Asn	Thr	Leu	Ile
				185					190					195
Ala	Asp	Tyr	Val	Ala	Lys	Ser	Gly	Phe	Phe	Arg	Val	Phe	Ile	Gly
				200					205					210
Val	Asn	Asp	Leu	Glu	Arg	Glu	Gly	Gln	Tyr	Met	Ser	Thr	Asp	Asn
				215					220					225
Thr	Pro	Leu	Gln	Asn	Tyr	Ser	Asn	Trp	Asn	Glu	Gly	Glu	Pro	Ser
				230					235					240
Asp	Pro	Tyr	Gly	His	Glu	Asp	Cys	Val	Glu	Met	Leu	Ser	Ser	Gly
				245					250					255
Arg	Trp	Asn	Asp	Thr	Glu	Cys	His	Leu	Thr	Met	Tyr	Phe	Val	Cys
				260					265					270
Glu	Phe	Ile	Lys	Lys	Lys	Lys	Lys							
				275										

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccataacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

ggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtgggtg 100

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

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cttggccttt gcggtgcgag ctctgtgctg caaaagggct cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccgg aaggtcccga ggggggctgc 450

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 catggcccaa cttgtttatt gcag 2574

<210> 102
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser
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 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly
 20 25 30
 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala
 35 40 45
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu
 50 55 60
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp
 65 70 75
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys
 80 85 90
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro
 95 100 105
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu
 110 115 120
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser
 125 130 135
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala
 140 145 150
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp
 155 160 165
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala
 170 175 180
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe
 185 190 195
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro
 200 205 210

Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315
Val	Pro	Gly	Tyr	Leu	Ser	Ser	Pro	Gln	Ser	Ile	Thr	Asp	Thr	Cys	320	325	330
Leu	Tyr	Ile	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	335	340	345
Arg	Ile	Ser	His	Leu	Lys	Ile	Leu	Gln	Cys	Gln	Gly	Phe	Tyr	Gln	350	355	360
Leu	Cys	Gly	Val	His	Gln	Glu	Asp	Val	Ile	Tyr	Leu	Ala	Leu	Pro	365	370	375
Leu	Tyr	His	Met	Ser	Gly	Ser	Leu	Leu	Gly	Ile	Val	Gly	Cys	Met	380	385	390
Gly	Ile	Gly	Ala	Thr	Val	Val	Leu	Lys	Ser	Lys	Phe	Ser	Ala	Gly	395	400	405
Gln	Phe	Trp	Glu	Asp	Cys	Gln	Gln	His	Arg	Val	Thr	Val	Phe	Gln	410	415	420
Tyr	Ile	Gly	Glu	Leu	Cys	Arg	Tyr	Leu	Val	Asn	Gln	Pro	Pro	Ser	425	430	435
Lys	Ala	Glu	Arg	Gly	His	Lys	Val	Arg	Leu	Ala	Val	Gly	Ser	Gly	440	445	450
Leu	Arg	Pro	Asp	Thr	Trp	Glu	Arg	Phe	Val	Arg	Arg	Phe	Gly	Pro	455	460	465
Leu	Gln	Val	Leu	Glu	Thr	Tyr	Gly	Leu	Thr	Glu	Gly	Asn	Val	Ala	470	475	480
Thr	Ile	Asn	Tyr	Thr	Gly	Gln	Arg	Gly	Ala	Val	Gly	Arg	Ala	Ser	485	490	495
Trp	Leu	Tyr	Lys	His	Ile	Phe	Pro	Phe	Ser	Leu	Ile	Arg	Tyr	Asp			

500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met	
515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser	
530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala	
545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe	
560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu	
575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu	
590	595	600
Asn Val Ala Thr Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp	
605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly	Val Thr Val Pro Gly His	
620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His	
635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu	
650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu	
665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn	
680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu	
695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr	
710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg	Ile	
725	730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 104
 ggagaatgtg gccacaac 18

 <210> 105
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 105
 gccctggcac agtgactcca tagacg 26

 <210> 106
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 106
 atccacttca gcggacac 18

 <210> 107
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 107
 ccagtgccag gatacctctc tccccccag agcataacag acacg 45

 <210> 108
 <211> 2579
 <212> DNA
 <213> Homo sapiens

 <400> 108
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 cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100

 acgcgcgcac acacactcgc tctcgtttgt ccattctcct cccgggggag 150

 ccggcgcgcg ctccacatt tgccgcacac tccggcgagc cgagcccgca 200

gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250
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 gcccttggtg gcttgccatc gtccatctgg cttataaaaag tttgctgagc 400
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 gacatcccct accaggagat cgcaggggaa cacttaagaa tctgtcctca 750
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 tgacttttgg gctcggctcc tggaaaggat gtttcagctg ataaaccctc 1100
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 attgtcctgg cactgcagag actgtgcaga taatcttggg tttttggtca 2250
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 cactcttgga caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350
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 ggggtgccaga ctgaactgct tctcttttcc ttcagctatc tgtggggacc 2450
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500
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 gtgaggggtt tttttttctc atttaaaat 2579

<210> 109
 <211> 555
 <212> PRT
 <213> Homo sapiens

<400> 109
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 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys
 20 25 30
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala
 35 40 45
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys
 50 55 60
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

365										370				375			
Ala	Ala	Gly	Thr	Ser	Leu	Asp	Arg	Leu	Val	Thr	Asp	Ile	Lys	Glu			
				380					385					390			
Lys	Leu	Lys	Leu	Ser	Lys	Lys	Val	Trp	Ser	Ala	Leu	Pro	Tyr	Thr			
				395					400					405			
Ile	Cys	Lys	Asp	Glu	Ser	Val	Thr	Ala	Gly	Thr	Ser	Asn	Glu	Glu			
				410					415					420			
Glu	Cys	Trp	Asn	Gly	His	Ser	Lys	Ala	Arg	Tyr	Leu	Pro	Glu	Ile			
				425					430					435			
Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp			
				440					445					450			
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met			
				455					460					465			
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly			
				470					475					480			
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser			
				485					490					495			
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe			
				500					505					510			
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg			
				515					520					525			
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser			
				530					535					540			
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg			
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<210> 110
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 110
 aagcgtgaca gcgggcacgt c 21

<210> 111
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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aataagttag ctgagaaaac gcacgcagtt tgcagcgctt gcgccgggtg 100

cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150

tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgctgcccgg agtttctgcg gaggtggagg gagatcagga aacggcttct 250

tctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300

aaaggactgg ggaaaatagc cctgggaaag tggagaaggt gatcaggagg 350

ccggtccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400

tccacttcgc agttctttcc aggtgtgggg accgcaggac agacggccga 450

tcccgcgcgc ctccgtacca gcactcccag gagagtcagc ctgcctcccc 500

aacgtcgagg gcgctctggc cacgaaaagt tcctgtccac tgtgattctc 550

aattccttgc ttgggttttt tctccagaga acttttgggt ggagatatta 600

acttttttct tttttttttt ccttgggtgga agctgctcta gggagggggg 650

aggaggagga gaaagtgaaa tgtgctggag aagagcgagc cctccttgtt 700

cttccggagt cccatccatt aagccatcac ttctggaaga ttaaagttgt 750

cggacatggt gacagctgag aggagaggag gatttcttgc caggtggaga 800

gtcttcaccg tctgttgggt gcatgtgtgc gccgcagcg gcgcggggcg 850

cgtggttctc cgcgtggagt ctcacctggg acctgagtga atggctccca 900

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4649

<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114
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 Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu
 20 25 30
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser
 35 40 45
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala
 50 55 60
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln
 65 70 75
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 80 85 90
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys
 95 100 105
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

110	115	120
Ile Cys Thr Pro Ser Arg Ser Gln Phe	Ile Thr Gly Lys Tyr Gln	
125	130	135
Ile His Thr Gly Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro	
140	145	150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	
155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	
170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	
185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	
200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	
215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	
230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	
245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	
260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	
275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405

Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
				410					415					420
Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
				425					430					435
Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
 cccaacccaa ctgtttacct ctgg 24

<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
gccaccctac ctcagaaact gaaggagggt ggntattcaa cgcatatggt 50
cgg 53

<210> 118
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086
<223> unknown base

<400> 118
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gccttgcgct cccgctgctg ctctcctggg tggcaggtgg ttccgggaac 200
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gagtgcgtgg gaccaaacia atgcagatgc tttccaggat acaccgggaa 400
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ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550
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tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800
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cctgggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaaacag 1000
catgaaaaag aaggcaaaaa ttaaaatgt taccacagaa cccaccagga 1050

ctctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100
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 actatcttta tatttgactt tgtatgtcag ttccctgggt tttttgatat 1850
 tgcacatag gacctctggc attttagaat tactagctga aaaattgtaa 1900
 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950
 caatatttgc tttaaatatc atatcactgt atcttctcag tcatttctga 2000
 atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050
 cctcngtata tctgatttgt atangtangt tgatngcctt ctctctacaa 2100
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgcct 2200
 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250
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<210> 119
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 119
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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

305

310

315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
 320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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gtgcagctgc tgcgttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatgggtg 150

tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200

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gctggaaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

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gcggtacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400
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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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			20						25					30
Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35						40					45
Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50						55					60
Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val
			65						70					75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly

80										85					90				
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr					
				95					100					105					
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr					
				110					115					120					
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile					
				125					130					135					
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser					
				140					145					150					
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn					
				155					160					165					
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser					
				170					175					180					
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser					
				185					190					195					
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln					
				200					205					210					
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile					
				215					220					225					
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro					
				230					235					240					
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala					
				245					250					255					
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe					
				260					265					270					
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys					
				275					280					285					

Thr Lys His Asp

<210> 125
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
 gcaatgaact gggagctgc 19

<210> 126
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggagg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

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 caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
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<210> 132
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 132
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 20 25 30
 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe
 35 40 45
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn
 50 55 60
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln
 65 70 75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
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Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

365										370				375			
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly			
				380					385					390			
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu			
				395					400					405			
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys			
				410					415					420			
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp			
				425					430					435			
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln			
				440					445					450			
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu			
				455					460					465			
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met			
				470					475					480			
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu			
				485					490					495			
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu			
				500					505					510			
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg			
				515					520					525			
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser			
				530					535					540			
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu			
				545					550					555			
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser			
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Cys

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

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<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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cctgaagacc cagtgggtggc actggtgggc accgatgcc cctgtgtctg 300

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gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct 450

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gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

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cttgtttgat gtgcacagcg tctgcgggt ggtgctgggt gcgaatggca 800

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 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950
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<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
	35	40	45
Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
	50	55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
	65	70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
	80	85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
	95	100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
	110	115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
	125	130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
	140	145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
	155	160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
	170	175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
	185	190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
	200	205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
	215	220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
	230	235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
	245	250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
	260	265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
	275	280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
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Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
305 310 315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgcgaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga gggtagtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
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<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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gtttaccctg ggcatcctgg aggctctcaa aggttggggac cagggttgga 450
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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			20						25					30

Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35						40					45

Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50						55					60

Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65						70					75

Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80						85					90

Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
			95						100					105

Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110						115					120

Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125						130					135

Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140						145					150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
			155						160					165

Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
			170						175					180

Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
			185						190					195

Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
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Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 146
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<210> 147
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 147
gcccagagca ggaggaatga tgagc 25

<210> 148
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 148
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
<211> 2196
<212> DNA
<213> Homo sapiens

<400> 149
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cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
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<210> 150
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 150
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 20 25 30
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp
 35 40 45
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His
 50 55 60
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys
 65 70 75
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu
 80 85 90
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro
 95 100 105
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu
 110 115 120
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg
 125 130 135
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu
 140 145 150
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser
 155 160 165
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val
 170 175 180
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp
 185 190 195
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro
 200 205 210
 Asp Asp Gly Ala Lys
 215

<210> 151

<211> 524
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 103, 233
<223> unknown base

<400> 151
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gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200
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tggagcgggt tcaagaccgc gtggagttct caggggaacc cagcaagtac 450
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
caactgctac atcatgaacc cccc 524

<210> 152
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
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<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cgctgcct gcaccttcaa ctctgtctac acagtgaacc acaaacagtt 50

<210> 156
<211> 2680
<212> DNA
<213> Homo sapiens

<400> 156
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<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
1				5					10					15
Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
			20						25					30
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
			35						40					45
Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
			50						55					60
Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
			65						70					75
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
			80						85					90
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
			95						100					105
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys

110					115					120				
Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135
Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150
Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165
Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180
Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195
Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210
Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225
Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240
Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
				245					250					255
Ile	Arg	Glu	Gln	Gln	Arg	Ser	Ala	Val	Ser	Thr	Ser	Trp	Leu	Leu
				260					265					270
Pro	Tyr	Asn	Tyr	Thr	Trp	Ser	Pro	Glu	Lys	Val	Phe	Val	Gln	Thr
				275					280					285
Pro	Thr	Ile	Asn	Tyr	Thr	Leu	Arg	Asp	Tyr	Arg	Lys	Phe	Phe	Gln
				290					295					300
Asp	Ile	Gly	Phe	Glu	Asp	Gly	Trp	Leu	Met	Arg	Gln	Asp	Thr	Glu
				305					310					315
Gly	Leu	Val	Glu	Ala	Thr	Met	Pro	Pro	Gly	Val	Gln	Leu	His	Cys
				320					325					330
Leu	Tyr	Gly	Thr	Gly	Val	Pro	Thr	Pro	Asp	Ser	Phe	Tyr	Tyr	Glu
				335					340					345
Ser	Phe	Pro	Asp	Arg	Asp	Pro	Lys	Ile	Cys	Phe	Gly	Asp	Gly	Asp
				350					355					360
Gly	Thr	Val	Asn	Leu	Lys	Ser	Ala	Leu	Gln	Cys	Gln	Ala	Trp	Gln
				365					370					375
Ser	Arg	Gln	Glu	His	Gln	Val	Leu	Leu	Gln	Glu	Leu	Pro	Gly	Ser
				380					385					390
Glu	His	Ile	Glu	Met	Leu	Ala	Asn	Ala	Thr	Thr	Leu	Ala	Tyr	Leu
				395					400					405

Lys Arg Val Leu Leu Gly Pro
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacggggc ctacttcctg gccctccgcg agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

cggacgcgtg ggcgacgcg tggggcggcg gcagcggcgg cgacggcgac 50

atggagagcg gggcctacgg cgcggccaaag gcggggcggt ccttcgacct 100

gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200

gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgccgctat ggcagtcca tcgggggtgct ggccttcctg gcctcggcct 300

tcttcttggt ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450
acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500
ttcagcttct tttccatctt ctctgggggt gtgctggcct ccctggccta 550
ccagcgctac aaggctggcg tggacgactt catccagaat tacgttgacc 600
ccactccgga cccaacact gcctacgcct cctacccagg tgcattctgtg 650
gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgagg 700
ctaccagccg cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750
cagagagggc cctccctct gccctggact ttcccatcag cctcctggaa 800
ctgccagccc ctctctttca cctgttccat cctgtgcagc tgacacacag 850
ctaaggagcc tcatagcctg gcgggggctg gcagagccac accccaagt 900
cctgtgcccga gagggttca gtcagccgt cactcctcca gggcactttt 950
aggaaagggg ttttagctag tgtttttct cgcttttaac gacctcagcc 1000
ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050
gcctcagctt cccccggcc cgggtcaggc cgtgggagcc gctattatct 1100
gcgttctctg ccaaagactc gtggggggcca tcacacctgc cctgtgcagc 1150
ggagccggac caggctcttg tgctcctact caggtttgct tcccctgtgc 1200
ccactgctgt atgatctggg ggccaccacc ctgtgccggt ggctctctgg 1250
ctgcctcccg tgggtgtagg gcggggctgg tgctcatggc acttctctct 1300
tgctcccacc cctggcagca gggaagggct ttgcctgaca acaccagct 1350
ttatgtaaatt attctgcagt tgttacttag gaagcctggg gagggcagg 1400
gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
tgggggagat gcccggcctg ggatgctggt tggagacgga ataaatgttt 1500
tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe
1 5 10 15

Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
20 25 30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	155	160	165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	170	175	180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	185	190	195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	200	205	210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		215	220	

<210> 163
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 tggctcttcgc cttgatcgtg ttct 24

<210> 164
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 164
 gtgtactgag cggcgggttag 20

<210> 165
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 165
 ctgaaggtga tggctgcct cac 23

<210> 166
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 166
 ccaggaggct catgggaaag tcc 23

<210> 167
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 167
 ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 168
 gagccaccta cctgtctccg aggccaggcc tgcagggcct catcggccag 50
 agggatgatca gtgagcagaa ggatgcccgt ggccgaggcc cccaggtgg 100
 ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
 atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
 cctggtgccc ctgtttgtgc tgetggccct gctcgtgctg gcttcggcgg 250
 ggggtgctact ctggtatttc ctaggggtaca aggcggaggt gatggtcagc 300
 caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350
 tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450
 aactccagct ccgtctattc ctttggggag ggacccctca cctgcttctt 500
 ctggttcatt ctccaaatcc ccgagcaccg ccggctgatg ctgagccccg 550
 aggtggtgca ggcactgctg gtggaggagc tgctgtccac agtcaacagc 600
 tcggctgccg tcccctacag ggccgagtac gaagtggacc ccgagggcct 650
 agtgatcctg gaagccagtg tgaaagacat agctgcattg aattccacgc 700
 tgggttgta cgcctacagc tacgtgggcc agggccaggt cctccggctg 750
 aaggggcctg accacctggc ctccagctgc ctgtggcacc tgcagggccc 800
 caaggacctc atgctcaaac tccggctgga gtggacgctg gcagagtgcc 850
 gggaccgact ggccatgtat gacgtggccg ggccctgga gaagaggctc 900
 atcacctcgg tgtacggctg cagccgccag gagcccgctg tggaggttct 950
 ggcgtcgggg gccatcatgg cggtcgtctg gaagaagggc ctgcacagct 1000
 actacgacce cttcgtgctc tccgtgcagc cggtggtctt ccaggcctgt 1050
 gaagtgaacc tgacgctgga caacaggctc gactcccagg gcgtcctcag 1100
 caccctgac tccccagct actactcgcc ccaaaccac tgctcctggc 1150
 acctcacggt gccctctctg gactacggct tggccctctg gtttgatgcc 1200
 tatgcactga ggaggcagaa gtatgatttg ccgtgcaccc agggccagtg 1250
 gacgatccag aacaggaggc tgtgtggctt gcgcacctg cagccctacg 1300
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 tcccagatct cctcaccgg gcccggtgtg cgggtgcact atggcttgta 1400
 caaccagtgc gaccctgcc ctggagagtt cctctgttct gtgaatggac 1450
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 gagagaaact gcgtttgcag agccacattc cagtgc aaag aggacagcac 1550
 atgcatctca ctgccaagg tctgtgatgg gcagcctgat tgtctcaacg 1600
 gcagcgatga agagcagtgc caggaagggg tgccatgtgg gacattcacc 1650
 ttccagtgtg aggaccggag ctgcgtgaag aagcccaacc cgcagtgtga 1700
 tgggaggccc gactgcaggg acggctcgga tgaggagcac tgtgactgtg 1750
 gcctccaggg cccctccagc cgcattgttg gtggagctgt gtcctccag 1800
 ggtgagtggc catggcaggc cagcctccag gttcggggtc gacacatctg 1850

tggggggggcc ctcacgcgtg accgctgggt gataacagct gccactgct 1900
 tccaggagga cagcatggcc tccacggatgc tgtggaccgt gttcctgggc 1950
 aagggtgtggc agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000
 ccgectgctc ctgcacccgt accacgaaga ggacagccat gactacgacg 2050
 tggcgctgct gcagctcgac caccgggtgg tgcgctcggc cgcggtgcgc 2100
 cccgtctgcc tgcccgcgcg ctcccacttc ttcgagcccg gcctgcactg 2150
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 ctctgcagaa agtggatgtg cagttgatcc cacaggacct gtgcagcgag 2250
 gcctatcgct accaggtgac gccacgcatg ctgtgtgccc gctaccgcaa 2300
 gggcaagaag gatgcctgtc aggggtgactc aggtgggtccg ctggtgtgca 2350
 aggcactcag tggccgctgg ttctggcgcg ggctgggtcag ctggggcctg 2400
 ggctgtggcc ggcctaacta cttcggcgctc tacaccgca tcacaggtgt 2450
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 gaggatggag aagtgccagc agctgggggt caagacgtcc cctgaggacc 2700
 caggcccaca cccagccctt ctgcctccca attctctctc ctccgtcccc 2750
 ttctccact gctgcctaata gcaaggcagt ggctcagcag caagaatgct 2800
 ggttctacat cccgaggagt gtctgaggtg cggccactc tgtacagagg 2850
 ctgtttgggc agccttgctt ccagagagca gattccagct tcggaagccc 2900
 ctggtctaac ttgggatctg ggaatggaag gtgctcccat cggagggggac 2950
 cctcagagcc ctggagactg ccaggtgggc ctgctgccac tgtaagccaa 3000
 aagggtggga agtctgact ccagggtcct tgccccaccc ctgcctgcca 3050
 cctgggcccct cacagcccag accctcactg ggaggtgagc tcagctgccc 3100
 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens
 <400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

290										295				300			
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val			
				305					310					315			
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu			
				320					325					330			
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro			
				335					340					345			
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His			
				350					355					360			
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp			
				365					370					375			
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln			
				380					385					390			
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile			
				395					400					405			
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly			
				410					415					420			
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly			
				425					430					435			
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro			
				440					445					450			
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys			
				455					460					465			
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys			
				470					475					480			
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile			
				485					490					495			
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly			
				500					505					510			
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe			
				515					520					525			
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro			
				530					535					540			
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu			
				545					550					555			
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly			
				560					565					570			
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu			
				575					580					585			

Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys	Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp	Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn	Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys	Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala	Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly	Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala	Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe	Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln	Val Val Thr		800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 170
 gcacccaggg ccagtggacg atccagaaca ggaggctgtg tggcttgccg 50
 atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100
 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccttg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250
 ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450
 ccaacccgca gtgtgatggg cggcccgaact gcagggacgg ctccgatgag 500
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550
 agctgtgtcc tccgaggggtg agtggccatg gcagggccagc ctccaggttc 600
 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650
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 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgcgtgg cctggagagg 750
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 agccatgact acgacgtggc gctgctgcag ctgcaccacc cggtggtgcg 850
 ctcgcccgcc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900
 agcccggcct gcactgctgg attacgggct ggggcgcctt gcgcgagggc 950
 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000
 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgctgt 1050
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150
 ggtcagctgg ggctggggct gtggccggcc taactacttc ggcgtctaca 1200
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
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 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc cactgcttc cagg 24

<210> 172

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 172
taatccagca gtgcaggccg gg 22

<210> 173
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tgcctatgca ctgaggaggc agaag 25

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
aggcagggac acagagtcca ttcac 25

<210> 176
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177
<211> 1510
<212> DNA
<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50
ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ctttctctgc 100
ctccagtecc ccagcccctg gccgagagaa gggctttacc ggccgggatt 150
gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200
ggaggggggtg tggcgggggca ggatgagcaa ctccgttcct ctgctctgtt 250
tctggagcct ctgctattgc tttgctgcgg ggagcccgt accttttggg 300
ccagaggggac ggctggaaga taagctccac aaacccaaag ctacacagac 350
tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450
tgcagtttca acatgacagc taaaaccttt ttcattcttc acggatggac 500
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550
acacaagaga gaaagacgcc aatgtagttg tgggtgactg gctccccctg 600
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agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400
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aaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

Ile Tyr Pro Asn	Gly Gly Asp Phe Gln	Pro Gly Cys Gly Leu Asn
245	250	255
Asp Val Leu Gly	Ser Ile Ala Tyr Gly	Thr Ile Thr Glu Val Val
260	265	270
Lys Cys Glu His	Glu Arg Ala Val His	Leu Phe Val Asp Ser Leu
275	280	285
Val Asn Gln Asp	Lys Pro Ser Phe Ala	Phe Gln Cys Thr Asp Ser
290	295	300
Asn Arg Phe Lys	Lys Gly Ile Cys Leu	Ser Cys Arg Lys Asn Arg
305	310	315
Cys Asn Ser Ile	Gly Tyr Asn Ala Lys	Lys Met Arg Asn Lys Arg
320	325	330
Asn Ser Lys Met	Tyr Leu Lys Thr Arg	Ala Gly Met Pro Phe Arg
335	340	345
Gly Asn Leu Gln	Ser Leu Glu Cys Pro	
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240
<212> DNA
<213> Homo sapiens

<400> 182

cgagcgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50
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acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150
cggcaaagtt tggcccgaag aggaagtggg ctcaaaccgc ggcaggtggc 200
gaccaggcca gaccaggggc gtcgctgcc tgcgggcggg ctgtaggcga 250
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agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
caccgcccct actcccgggc tgccgcgcgc tccccgcccc cagccctggc 400
atccagagta cgggtcgagc ccgggccatg gagccccct ggggaggcgg 450
caccagggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500
ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
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 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183
 <211> 713
 <212> PRT
 <213> Homo sapiens

<400> 183
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 20 25 30
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro
 35 40 45
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu
 50 55 60
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys
 65 70 75
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro
 80 85 90
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu
 95 100 105
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly
 110 115 120
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln
 125 130 135
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His
 140 145 150
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys
 155 160 165
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

170					175					180				
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr
				185					190					195
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His
				200					205					210
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp
				215					220					225
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp
				230					235					240
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro
				245					250					255
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn
				260					265					270
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val
				275					280					285
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala
				290					295					300
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys
				305					310					315
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg
				320					325					330
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala
				335					340					345
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His
				350					355					360
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr
				365					370					375
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly
				380					385					390
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg
				395					400					405
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly
				410					415					420
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr
				425					430					435
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu
				440					445					450
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys
				455					460					465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu	470	475	480
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser	485	490	495
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp	500	505	510
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu	515	520	525
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly	530	535	540
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg	545	550	555
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn	560	565	570
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser	575	580	585
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg	590	595	600
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro	605	610	615
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala	620	625	630
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro	635	640	645
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly	650	655	660
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro	665	670	675
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp	680	685	690
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu	695	700	705
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr								710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
 ggctgtcact gtggagacac 20

<210> 185
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 185
 gcaaggtcat tacagctg 18

<210> 186
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 186
 agaacatagg agcagtccca ctc 23

<210> 187
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 187
 tgcctgctgc tgcacaatct cag 23

<210> 188
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 188
 ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
 <211> 663
 <212> DNA
 <213> Homo sapiens

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 gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100
 gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
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gccccgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
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agttgggtgga ggggtgtttg cacttggtgac agcagtatgc tgtcttgccg 500
acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
aaaaaaaaaa aaa 663

<210> 190
<211> 152
<212> PRT
<213> Homo sapiens

<400> 190
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Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
35 40 45
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
50 55 60
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
65 70 75
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
80 85 90
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
95 100 105
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
110 115 120
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
125 130 135
Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 212, 234, 487
<223> unknown base

<400> 191
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catcgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
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atacttttat atgtactcag acttgatcga ttaatgaagt gggtattttg 350
gccttttgctt gatattatca actcactggg aacaacagta ttcattgctca 400
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ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cgttttgcag aacctactca ggcag 25

<210> 193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 193
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194
<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgtgagc cgcggtgcc ggacgggacg 50

ggaccggcta ggctgggccc gccccccggg ccccgccgtg ggcatgggcg 100

cactggcccc ggcgtgtgtg ctgcctctgc tggcccagtg gtccttgcgc 150

gccgccccgg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200

cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccttg 250

ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccttggcg 300

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ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400

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cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550

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 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196
 <211> 518
 <212> PRT
 <213> Homo sapien

<400> 196
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 20 25 30
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 35 40 45
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
 50 55 60
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala
 65 70 75
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg
 80 85 90
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	335	340	345
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	350	355	360
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	365	370	375
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	380	385	390
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu			

	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg	485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser	500	505	510
Ser Leu Val Arg His Arg Trp Lys	515		

<210> 197
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 197
 cgcagaagct acagattctc g 21

<210> 198
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 198
 ggaaattgga ggccaaagc 19

<210> 199
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 199
 ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggctc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA

<213> Homo sapiens

<400> 205

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 taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 206
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 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly
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 35 40 45
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile
 80 85 90
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe
 95 100 105
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
 110 115 120
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe
 125 130 135
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr
 140 145 150

His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	365	370	375
Leu	Ser																

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208
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<223> Synthetic oligonucleotide probe

<400> 208
acgccagtgg cctcaagctg gttg 24

<210> 209
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 209
ctttctgagc tctgagccac ggttgacat cctcatccac aatgc 45

<210> 210
<211> 3716
<212> DNA
<213> Homo sapiens

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aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
				20					25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420
Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu			

530										535				540			
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp			
				545					550					555			
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser			
				560					565					570			
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu			
				575					580					585			
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp			
				590					595					600			
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu			
				605					610					615			
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln			
				620					625					630			
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu			
				635					640					645			
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser			
				650					655					660			
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala			
				665					670					675			
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg			
				680					685					690			
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr			
				695					700					705			
Gln	Ser	Gln	Gln	Thr	Gln	Pro	Pro	Val	Ala	Pro	Gln	Ala	Pro	Ser			
				710					715					720			
Ser	Ile	Leu	Leu	Pro	Ala	Ala	Pro	Ile	Pro	Ile	Leu	Ser	Pro	Cys			
				725					730					735			
Ser	Pro	Pro	Ser	Pro	Gln	Ala	Ser	Ser	Leu	Ser	Gly	Pro	Ser	Pro			
				740					745					750			
Ala	Ser	Ser	Arg	Leu	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Leu	Gly	Glu			
				755					760					765			
Asp	Gln	Asp	Ser	Val	Leu	Thr	Pro	Glu	Glu	Val	Ala	Leu	Cys	Leu			
				770					775					780			
Glu	Leu	Ser	Glu	Gly	Glu	Glu	Thr	Pro	Arg	Asn	Ser	Val	Ser	Pro			
				785					790					795			
Met	Pro	Arg	Ala	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Gly	Tyr	Ile	Ser			
				800					805					810			
Val	Pro	Thr	Ala	Ser	Glu	Phe	Thr	Asp	Met	Gly	Arg	Thr	Gly	Gly			
				815					820					825			

Gly Val Gly Pro	Lys Gly Gly Val Leu	Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro	Thr Pro Ser Glu Gly	Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser	Glu Asp Asn Ala Ala	Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser	Asp Gly Ser Phe Leu	Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala	Val Ala Val Asp Ser	Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala	Asp Cys Val Phe Ile	Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp	Glu Ile Phe Leu Thr	Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp	Arg Pro Asp Trp Leu	Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg	Leu Gly Arg Gly Met	Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser	Ser Gln Arg Ser Gln	Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala	Ser Pro Val Asp Tyr	Ser	980	985	

<210> 212

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 212

gaagggacct acatgtgtgt ggcc 24

<210> 213

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 213

actgaccttc cagctgagcc acac 24

<210> 214

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgogg cttctgggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta caggggaagag 150

ctgagggacc accggaagta ctggtgcagg aaggggtggga tcctcttctc 200

tcgctgtctt ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggggt 350

cgaaaaacgg ggccccgatg agtcttttact gatctctctg ttcgtctttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctgggt 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccag 500

attgacttct cctgggtctt acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggccctt ccattgccag ggacttccca gtacgggcac 600

gaaaggactt ctcaatcac aggaacctct cctcaccag cgacctctcc 650

tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc caggggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggcttgatcg cttctgcag ccacctgctc ctgtggagaa 850

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tctttttaca gagcaattat cttgtatata caactttgta tcttgccctt 2650
tccaccttat cgttccatca ctttattcca gcacttctct gtgtttttaca 2700
gaccttttta taaataaaaat gttcatcagc tgcataaaaa aaaaaaaa 2749

<210> 216
<211> 332
<212> PRT
<213> Homo sapiens

<400> 216
Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
1 5 10 15
Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
20 25 30
Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp
35 40 45
His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
50 55 60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met
65 70 75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu
80 85 90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
95 100 105
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
110 115 120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
125 130 135
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
140 145 150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
155 160 165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
170 175 180
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
185 190 195
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

	200		205		210
Ala Gly Ser Ser Arg Pro Pro Met Gln	215		Leu Asp Ser Thr Ser	220	Ala 225
Glu Asp Thr Ser Pro Ala Leu Ser Ser	230		Gly Ser Ser Lys Pro Arg	235	240
Val Ser Ile Pro Met Val Arg Ile Leu	245		Ala Pro Val Leu Val Leu	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu	260		Ile Ala Phe Cys Ser His	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln	275		Gln Ala Thr Glu Thr Gln	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg	290		Leu Thr Ala Glu Glu Lys	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly	305		Asp Val Ile Ser Met Pro	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu	320		Gly Phe Ser Lys Phe Val	325	330

Ser Ala

<210> 217

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 217

ccctgcagtg cacctacagg gaag 24

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 218

ctgtcttccc ctgcttggt gtgg 24

<210> 219

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 219
ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtgga 100
cagtgtgaaa gaaccagtgg tctcgctctg ttgcccaggc tagagtgtac 150
tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagtgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400
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tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
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gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
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gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221
<211> 146
<212> PRT
<213> Homo sapiens

<400> 221
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser
1 5 10 15
Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu
20 25 30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp	35	40	45
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala	50	55	60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln	65	70	75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro	80	85	90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu	95	100	105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln	110	115	120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys	125	130	135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe					140	145	

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

gggatcatgt tggtggccct ggctc 24

<210> 223

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcaaggcaga cccagtcagc cag 23

<210> 224

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 224

ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225

agccgctgcc ccggggccggg cgcccgcggc ggcaccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tctctgtctt cgccgtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctcgggtgcgc cgcgggtgcc 250
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctt ggcaagggtg tgacgcaagg 350
gactcgggag gcgcccttcg tgtacgccat ctcttcggca ggtgtggcct 400
ttgcagtgc gggggcgtgc agcagtgggg agctggagaa gtgcggctgt 450
gacaggacag tgcatggggg cagcccacag ggcttcaggt ggtcaggatg 500
ctctgacaac atcgctacg gtgtggcctt ctacagtcg tttgtggatg 550
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atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700
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gatggtgcca ctgagggtgga gccacgccgc gtgggctcct ccagggcact 800
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acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900
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aaacagtctc ccaccacctc cccaagaga tactggttgt attttttgtt 1200
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gctgccactg accactcagt tggtatctgt gtccggtttt ctacttgag 1400
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 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccc 1850
 gctgtgcctt tgcagtcag cccgagtcac ctttcacagc gctgttcctc 1900
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
 acacacacac ggacacacac acacacctgc gagagagagg gaggaagg 2000
 ctgtgccttt gcagtcagc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
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Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro	215	220	225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly	230	235	240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu	245	250	255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu	260	265	270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg	275	280	285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser	290	295	300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe	305	310	315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe	320	325	330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val	335	340	345
Glu	Leu	His	Thr	Cys	Arg										350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 228
tgggtgggaga ctgttttaaatt tatcggcc 28

<210> 229
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 229
tgcttcgtca agtgccggca gtgccagcgg ctcgtggagt t 41

<210> 230
<211> 1355
<212> DNA
<213> Homo sapiens

<400> 230
cggacgcgtg ggccggacgcg tgggcccggacg cgtgggcccga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
gcgccgctgg gtgccctgaa ggaggaggctc ggagactgcc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500
cactgagctg ttccggggcg tggaggccgt gaggctccag aacaactcct 550
gcgagccgtg cccacgctc tggctgtcct tcgagggctc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcccgg gcgcaggatc actgcgcaga 650
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
tcactcgga cagcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000
gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050
tcctcatcca ccgctgctga gtctcagaaa cacttggtccc aacatagccc 1100
tgtccagccc agtgcctggg ctctgggacc tccatgccga cctcatccta 1150
actccactca cgcagacca acctaacctc cactagctcc aaaatccctg 1200
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggttag 1250
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
aaaaa 1355

<210> 231
<211> 293
<212> PRT
<213> Homo sapiens

<400> 231
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
1 5 10 15
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
20 25 30
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
35 40 45
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
50 55 60
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
65 70 75
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
80 85 90
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
95 100 105
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
110 115 120
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	
				140					145					150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	
				155					160					165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
				170					175					180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	
				185					190					195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	
				200					205					210	
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	
				215					220					225	
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	
				230					235					240	
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	
				245					250					255	
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	
				260					265					270	
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	
				275					280					285	
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								
				290											

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctccctcttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggccgccgcg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450

gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctggggggccg 500

cgcatagtc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggagggtg 700

cagcgcaggc actcgttggt ctcgtttggt gtgcgcacgt tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca ccttctctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcata cctcccgcgc cagtccctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100

tggactgcga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150
 tgtggggaggc tggggaccaa gagcaggact cgctacgtcc ggggtccagcc 1200
 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250
 tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggccccc 1300
 cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350
 ccgagggcac aggggggtttc gcgctgtctc tgaccgcggt gaggccgcgc 1400
 cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
 aaacagcctc ctcccttccc aaccttgctt cttagggggc cccgtgtccc 1500
 gtctgtctc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550
 cagctactct aaattatgtc tcttataag ttattgtgc tccaggagat 1600
 tgtccttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650
 gacctggtgc tctaggctgt gctgagccca ctctcccag ggcgcatcca 1700
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys
 1 5 10 15
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly
 20 25 30
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile
 35 40 45
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr
 50 55 60
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
 65 70 75
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val
 80 85 90
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala
 95 100 105
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val

110					115					120				
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165
Asp	Ser	Leu	Asp	Leu	Cys	Asp	Gly	Asp	Arg	Trp	Arg	Glu	Gln	Ala
				170					175					180
Ala	Leu	Asp	Leu	Tyr	Pro	Tyr	Asp	Ala	Gly	Thr	Asp	Ser	Gly	Phe
				185					190					195
Thr	Phe	Ser	Ser	Pro	Asn	Phe	Ala	Thr	Ile	Pro	Gln	Asp	Thr	Val
				200					205					210
Thr	Glu	Ile	Thr	Ser	Ser	Ser	Pro	Ser	His	Pro	Ala	Asn	Ser	Phe
				215					220					225
Tyr	Tyr	Pro	Arg	Leu	Lys	Ala	Leu	Pro	Pro	Ile	Ala	Arg	Val	Thr
				230					235					240
Leu	Leu	Arg	Leu	Arg	Gln	Ser	Pro	Arg	Ala	Phe	Ile	Pro	Pro	Ala
				245					250					255
Pro	Val	Leu	Pro	Ser	Arg	Asp	Asn	Glu	Ile	Val	Asp	Ser	Ala	Ser
				260					265					270
Val	Pro	Glu	Thr	Pro	Leu	Asp	Cys	Glu	Val	Ser	Leu	Trp	Ser	Ser
				275					280					285
Trp	Gly	Leu	Cys	Gly	Gly	His	Cys	Gly	Arg	Leu	Gly	Thr	Lys	Ser
				290					295					300
Arg	Thr	Arg	Tyr	Val	Arg	Val	Gln	Pro	Ala	Asn	Asn	Gly	Ser	Pro
				305					310					315
Cys	Pro	Glu	Leu	Glu	Glu	Glu	Ala	Glu	Cys	Val	Pro	Asp	Asn	Cys
				320					325					330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 238
caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagcccttc tctctcttcc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcacccgt gtcctgcggg atg.23

<210> 243
<211> 42
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50

tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100

aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150

tcaccccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200

tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250

gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300

cagaaatddd atccaacttt gtttggaagc ttattatgac aataccattt 350

ttcatagagt tgtgcctggg ttcatagtcc aaggcggaga tctactggc 400

acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450

tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaattg 500

ctggttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550

gatgaactta acaataagca taccatcttt ggaaagggtta caggggatac 600

agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650

gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaattcct 700

tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750

agaggaggaa gttaaagaaat tgaaacccaa aggcacaaaa aattttagtt 800

tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaattcga 850

gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900

ggatgatcca catctcagtt ctgttccagt tgtagaaagt gaaaaagggtg 950

atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000

gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050

aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100

aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gccccctccag 1250
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aggaagcaac agtcaaagaa gggaacttcc cgggaagatc agacccttgc 1350
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ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500
catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600
agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650
acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700
gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750
tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
catgtgtttt ttcttagctg accttttata ttgctaaatc tgaaataaaa 1850
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val
1				5					10					15
Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
				20					25					30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
				35					40					45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
				50					55					60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
				65					70					75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
				80					85					90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
				95					100					105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	
				110					115					120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	
				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
				200					205					210	
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	
				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
				290					295					300	
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
				305					310					315	
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
				320					325					330	
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
				335					340					345	
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
				350					355					360	
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
				365					370					375	
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
				380					385					390	
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp Met	
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys Asp	
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro Arg	
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu	Glu Ser Lys Lys Leu Met	
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249
 caactggaac aggaactgag atgtggatc 29

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 251
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 cctctccgat taaaacgc 18

<210> 252
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 252
 gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
 <211> 2456
 <212> DNA
 <213> Homo sapiens

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 catttcgctt tgctgacggc gtgcagccct ggccagacat gtccacaggg 150
 ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgcccggcg 200
 gaccagcaca ggcggcgttt tctccttcgg aacgggaacg tctagcaacc 250
 cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300
 actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350
 acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400

ccaagaggcc tcaagtggtc accaaatatg gaaccctgca aggaaaacag 450
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 ttattcagac ttttcatcac tagtaaccca ctgaaagtgg ccaagaagg 1250
 tgcccacctg gctggatgca accacaacag cacacagatc ctggtaaact 1300
 gcctgagggc actatcaggg accaagggtga tgcgtgtgtc caacaagatg 1350
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 catgagccct gtggtggatg gtgtggtgat cccagatgac cttttggtgc 1450
 tctgacceca ggggaagggt tcatctgtgc cctaccttct aggtgtcaac 1500
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 tttggatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850

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 gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254

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Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly	35	40	45	
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser	50	55	60	
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly	65	70	75	
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg	80	85	90	
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met	95	100	105	
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe	110	115	120	
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro	125	130	135	

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	
				140					145					150	
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	
				155					160					165	
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	
				170					175					180	
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	
				185					190					195	
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	
				200					205					210	
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	
				215					220					225	
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	
				230					235					240	
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	
				245					250					255	
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	
				260					265					270	
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	
				275					280					285	
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	
				290					295					300	
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	
				305					310					315	
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	
				320					325					330	
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	
				335					340					345	
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	
				350					355					360	
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	
				365					370					375	
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	
				380					385					390	
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	
				395					400					405	
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	
				410					415					420	
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro	

425	430	435
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440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr	Asn
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val	Val Glu Glu Tyr Leu	Asp
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met	Leu Arg Asn Arg Met	Met
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr	
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala	
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu	
530	535	540
Pro Gln Glu Trp Ala		
545		

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 256
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257
 gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258
<211> 2764
<212> DNA
<213> Homo sapiens

<400> 258
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actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100
ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150
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aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
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caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550
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 cccaaaaggg ggaggaatga ataatccacc ccttgtttag caaataagca 2650
 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700
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tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225
Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
				230					235					240
His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
				245					250					255

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
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Val	Lys	Phe	Gln												

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 261
ttctggagcc cagaggggtgc tgag 24

<210> 262
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263
<211> 2857
<212> DNA
<213> Homo sapiens

<400> 263
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caacagaaaa ctctcaaca aagaaagtca agcagccagt gcgatctcat 150
ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200
aatgaatacg actagtcac acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

toggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
 cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
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 cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700
 taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750
 acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800
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 ttccatatta tgtatttgaa gtttttgaag aaaccacaca gggatcattt 1200
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 tcactacaag taactcactg gatcgtgaaa tcagtgttg gtacaaccta 1350
 agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400
 actgtatgtg caagttctta acatcaatga tcatgtcct gagttctctc 1450
 aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500
 cagactatca gtgcagtgga tagagatgaa tccatagaag agcaccattt 1550
 ttactttaat ctatctgtag aagacactaa caattcaagt tttacaatca 1600
 tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650
 aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700
 tggaatcccg tcacttaca gtacaaacac ccttaccatc catgtctgtg 1750
 actgtgggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800
 ctttccatgg gattcaagac agaagttatc attgctattc tcatttgcac 1850
 tatgatcata tttgggttta ttttttgac tttgggttta aaacaacgga 1900

gaaaacagat tctatttcct gagaaaagtg aagatttcag agagaatata 1950
 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200
 cttttgaggg aacaggggtca ttagctggat ccctgagctc cttagaatca 2250
 gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300
 tcgctttaaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350
 attagggctt tttaccatca aaatttttaa aagtgcataat gtgtattcga 2400
 acccaatggg agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450
 agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500
 ttatttttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550
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 aatgtaggaa gatattaaaa gtatgagaga ggacacaaga ttagtcgat 2650
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700
 cgagaaaatt taaaggagca aaaatttgca agtcaaataa aaatgtacaa 2750
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
 atttaaa 2857

<210> 264
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 264
 Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu
 1 5 10 15
 Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys
 20 25 30
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp
 35 40 45
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser
 50 55 60

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
				170					175					180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
				290					295					300	
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
				305					310					315	
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr	
				320					325					330	
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	

350										355				360			
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr			
				365					370					375			
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly			
				380					385					390			
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg			
				395					400					405			
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly			
				410					415					420			
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp			
				425					430					435			
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln			
				440					445					450			
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp			
				455					460					465			
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu			
				470					475					480			
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp			
				485					490					495			
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser			
				500					505					510			
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln			
				515					520					525			
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu			
				530					535					540			
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn			
				545					550					555			
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val			
				560					565					570			
Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln			
				575					580					585			
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala			
				590					595					600			
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr			
				605					610					615			
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys			
				620					625					630			
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly			
				635					640					645			

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 24, 60, 141, 226, 228, 249, 252
 <223> unknown base

<400> 265
 atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50
 gaatattnn taaaatggat agagaactgc aagatgagta ttgggtaatc 100
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgcgcgcccc gggcgcggaac 50

cccaaccccc acccagagct tctccagcgg cggcgcagcg agcaggggtc 100

ccgccttaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcag ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300

ccagtgagg gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtggttggca tcctcctggg agtgatagca 500

atctttgtgg ccaccgttgg catgaagtgt atgaagtgtc tggaagacga 550

tgagggtgcag aagatgagga tggctgtcat tgggggtgca atatttcttc 600

ttgcaggctt ggctatttta gttgccacag catgggatgg caatagaatc 650
 gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700
 tggtcaggct ctcttcactg gctgggctgc tgcttctctc tgccttctgg 750
 gaggtgccct actttgctgt tctgtcccc gaaaaacaac ctcttaccga 800
 acaccaaggc cctatccaaa acctgcacct tccagcgga aagactacgt 850
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
 aatctgaagt atgggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
 gttaaaatac tcagtgtctaa acatggctta atcttatttt atcttctttc 1050
 ctcaatatag gaggggaagat ttttccattt gtattactgc ttcccattga 1100
 gtaatcatat tcaaattgggg gaaggggtgc tccctaaata tatatagata 1150
 tgtatatata catgtttttc tattaanaat agacagtaaa atactattct 1200
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
 atttaattcc atattgatga agatgtttat tgggtatattt tctttttcgt 1300
 ccttatatac atatgtaaca gtcaaatac atttactctt cttcattagc 1350
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 tttcaattct tcatgctgc ccttttcata tacttatttt attttttacc 1450
 ataattctat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500
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 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600
 tctttctgca tgaccaaagt gataaattcc tgttgacctt cccacacaat 1650
 ccctgtactc tgacccatag cactcttggt tgctttgaaa atatttgtcc 1700
 aattgagtag ctgcatgctg ttccccagg tgttgtaaca caactttatt 1750
 gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800
 ctttttggtc cccattcctt aattgtattg ttttcccaag tgtaattatc 1850
 atgcgtttta tatcttcta ataagggtgtg gtctgtttgt ctgaacaaag 1900
 tgctagactt tctggagtga taatctggtg acaaattatc tctctgtagc 1950
 tgtaagcaag tcacttaatc tttctacctc ttttttctat ctgccaaatt 2000
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100
 tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150
 acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctattt 2200
 ccactgaaca aaacctacac acataccttc atgtgggttca gtgccttcct 2250
 ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300
 gtggctcagt gccttcctct ctctaccagt ctatttccat tctttcagct 2350
 gtgtctgaca tgtttgtgct ctgttccatt ttaacaactg ctcttacttt 2400
 tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450
 aggggtgttg cactgggtgc tggagacctg gatttgagtc ttggtgctat 2500
 caatcacctg ctgtgtttga gcaaggcatt tggtgctgt aagcttattg 2550
 cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600
 gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650
 atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
 gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaaa tgttaag 2747

<210> 270
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 270
 Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe
 1 5 10 15
 Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp
 20 25 30
 Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala
 35 40 45
 Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly
 50 55 60
 Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser
 65 70 75
 Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu
 80 85 90
 Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met
 95 100 105
 Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val
 110 115 120

Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val
				125					130					135
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp
				140					145					150
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu
				155					160					165
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala
				170					175					180
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr
				185					190					195
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr
				200					205					210

Val

<210> 271
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 21, 69, 163, 434, 436, 444
 <223> unknown base

<400> 271
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 ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatgggtgg tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acantttctat 450
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggctctctt 500
 cactggctgg gctgctgctt ctctctgctt tctgggaggt gccctacttt 550
 gctgttcctg tccc 564

<210> 272
 <211> 498

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341
<223> unknown base

<400> 272
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200
tcgcagagca cggggcagat ccagtgc aaa gtctttgact cccttgctga 250
atctgagcag cacattgcaa gcaacccgtg ccttgatggg ggttggcacc 300
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgtg 350
tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
gggggcgcga tatttcttct tgcaggtctg gctattttag ttgccacagc 450
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273
<211> 552
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273
gggcccgcacc attatccaac cgggntcact gttgggtcat ctcccctctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttncctat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtgggtg 250
gcacccctct gggagtgaata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgcagg tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450

cccagtcaat gccaggtacg aatttggtca ggctctcttc actggtggtg 500

ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttctgc 550

ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

atttccccct cctggatgga tgcncacc gtcacattgc cttccccan 50

tggaggattn actcctatgc tggcgacaac atcgtgaccc ccaggccat 100

ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150

ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200

caaccctgct cttgatgggg ttggcatcct cctgggagtg atagcaacct 250

ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300

gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350

caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400

cnngnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500

gtgcctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50

gcagcacatt ncaagcaacc ccttgcttg aagggtggtg ncatcccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300
 tgccaggtac gaatttggtc aggctctctt cactggctgg gctgctgctt 350
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
 <223> unknown base

<400> 276
 agcaatgcc tgcgccaggt ggaggattaa ttcctatgnt ggggacaaca 50
 ttgtgacngc ccaggccatg tacggggggc tgtggatgct ctgcgtgtcg 100
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggt ggcatcttcc 200
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
 cgcgatattt cttnttgcag gtctggctat tttagttgcc acagcatggt 350
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400
 gccaggtacg aatttggtca ggctttnttc actggctggg ctgctgcttn 450
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 87, 138, 147, 163, 165-166, 172
 <223> unknown base

<400> 277
 tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50
 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100
 cccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278
<211> 542
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396
<223> unknown base

<400> 278
ttcctgggat ggatccgccc ccactntcac atgccctgcc ccttgagat 50
ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150
aagtctttga ctcttgctg aatctgagca gcacattgca agcaacctg 200
ccttgatggt gggtggcatc ctctgggag tgatagcaat ctttgtggcc 250
accgttggca tgaaagtgt tgaagtgtt ggaagacgat gaggtgcaga 300
agatgaggat ggctgtcatt gggggcgcga tttttcttct tgcaggctctg 350
gctatttttag nngccacagc atgggtatggc aatcagaccc nntcanaaac 400
tctatgaccc tatgaccca gtcaatgcc ggtacgaatt tggtcaggct 450
ctcttcactg gctgggctgc tgcttctctc tgcttcttgg gaggtgcct 500
actttgctgt tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctgttgggc ttcactctgc ttcctgggat ggaatcggcg 50
ccatcgtcag cactgcctg cccatggag gatttactcn tatgtggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200
aatctgagca gcacattgca agcaacctg ccttgatggt gggtggcatc 250
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgtctg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
 atgggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
 tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
 gcttctctct gccttctggg aggtgcccta ctttgcctgt cctgcgaa 548

<210> 280
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 280
 cgagcgagtc atggccaacg c 21

<210> 281
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 281
 gtgtcacacg tagtctttcc cgctgg 26

<210> 282
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 282
 ctgcagctgt tgggcttcat tctcgccctc ctgggatgga tcg 43

<210> 283
 <211> 2285
 <212> DNA
 <213> Homo sapiens

<400> 283
 gcgtgccgtc agctcgccgg gcaccgcggc ctcgccctcg cctccgccc 50
 ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100
 tagaggaccc ccgcccgtgc ccgacccgt ccccgccctt ttgtaaaact 150
 taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200
 ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250
 ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

cccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350
 gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
 caacagcggga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
 tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
 gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
 gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
 ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
 attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700
 tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
 gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800
 ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850
 ccccatTTca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
 ggctcttggc tctgggtggt ttgttcttta tegtgtgtgt aattattggg 950
 aagattgcct ttagaggta gcatgcacag gatggtaa at tggattggtg 1000
 gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050
 aattaatgta tgatgacatc tcacaggtct tgcctttaa ttaccctcc 1100
 ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
 ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
 ctttattaat gacaaggga accatgagta atgccacaat ggcatattgt 1250
 aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
 tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc cttggggag 1350
 ctggagccca gcatgctggg gagtgcggtc agctccacac agtagtccc 1400
 acgtggccca ctcccggccc aggtgcttt ccgtgtcttc agttctgtcc 1450
 aagccatcag ctcttggga ctgatgaaca gagtcagaag cccaaaggaa 1500
 ttgcactgtg gcagcatcag acgtactcgt cataagtga aggcgtgtgt 1550
 tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttact 1600
 taaagggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650
 ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatt 1700
 catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750

ctctgttggg tgaactggta ttgctgctgg agggctgtgg gctcctctgt 1800
 ctctggagag tctggatcatg tggaggtggg gtttattggg atgctggaga 1850
 agagctgcc a ggaagtgtt tttctgggtc agtaaataac aactgtcata 1900
 gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ctttttttaa 1950
 tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
 actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
 ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
 gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150
 tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
 atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250
 agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 284
 Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu
 1 5 10 15
 Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu
 20 25 30
 Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys
 35 40 45
 Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile
 50 55 60
 Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro
 65 70 75
 Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val
 80 85 90
 Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val
 95 100 105
 Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg
 110 115 120
 Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val
 125 130 135
 Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr
 140 145 150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

<210> 285
 <211> 418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 40, 53, 68, 119, 134, 177-178, 255
 <223> unknown base

<400> 285
 gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50
 tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
 cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
 cttctagtag tagttgagag tttagactgtg aattaatttt atgccataaa 250
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
 gttaacttta aaatgagc 418

<210> 286
 <211> 543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaatgaca ccnttcctcg cctgttggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata ttttaacttat ttaatgtatt 450
tcattctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctgggtggt tttgttcttt aattcggttg tgtaattntt gggaagattg 50
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaat ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288
 ggtggcccat tcccggccca ggctgcttcc cggtnttcag ttctgtccaa 50
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
 gcaactgtggc agcatnagac gtacttgtna taagtgaag gctgtgttg 150
 actgattgac ccagcgcttt ggaaataaat ggcagtgcctt tgttcantta 200
 aagggaccaa gctaaatttg tattgggttca tgtagtgaag tcaaactgtt 250
 attcagagat gtttaatgca tatttaantt atttaaatgta tttnatntca 300
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 289
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
 tactcgtcat aagtgaaggg cgtgtgttga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gttcacttaa agggaccaag cttaaattgt 200
 attgggtcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598
 <223> unknown base

<400> 290
 aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
 gaaacntgn gtaatgccac aatggcatat tgtaaagtgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
 cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400
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 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550
 acaagggtac agttaatgct gcgtgctgct gaantctggt gggatgaantg 600
 gtattgctg 609

<210> 291
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 291
 ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50
 cacagtagtc cccacgtggc ccactcccgg cccaggctgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
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 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctggt gggatgaactg gtattgctgc tggagggctg 450
 tgggctcctc tgtctctgga gagtctgggc atgtggaggt ggg 493

<210> 292
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 292
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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ggctggctga gaggtccca gctgcagcgt ccccgccgc ctccctcgga 100

gctctgatct cagctgacag tgcctcggg gaccaaaca gcctggcagg 150

gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atctttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350

atcttatgtg gcacttgaga aaggtaaccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650

gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850

aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagaggggtac cagagagcat ctgcaggaga 950
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actatgctct tctggagctg aagcgtgctc acaaaaagaa atacatggaa 1150
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gtgggcactt caatgccaa tatatactct tctttacatg gtgatgagtt 1750
tcattttagt aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800
accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850
ctcagggtcc tactctaaga agaataaat aggatgctgg ttgtgtatta 1900
aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
atagagacag aaagttacaa cacagtgtgt actactctga gatggatcca 2000
ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctctggga 2050
catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200
cctagtttag aaataggga gctgagacat ttaagatct caagttttta 2250
tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300

cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctaaaaatg aataaaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

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1				5					10					15	
Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	
			20						25					30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	
			35						40					45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	
			50						55					60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	
			65						70					75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	
			80						85					90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	
			95						100					105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	
			110						115					120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	
			125						130					135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	
			140						145					150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	
			155						160					165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	
			170						175					180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	
			185						190					195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	
			200						205					210	

Ser Gly Gly Asp	Gln Arg Glu Gly Thr	Arg Glu His Leu Gln Glu
215	220	225
Arg Ala Lys Gly	Gly Arg Arg Arg Lys	Lys Ser Gly Arg Gly Gln
230	235	240
Arg Ile Ala Glu	Gly Arg Pro Ser Phe	Gln Trp Thr Arg Val Lys
245	250	255
Asn Thr His Ile	Pro Lys Gly Trp Ala	Arg Gly Gly Met Gly Asp
260	265	270
Ala Thr Leu Asp	Tyr Asp Tyr Ala Leu	Leu Glu Leu Lys Arg Ala
275	280	285
His Lys Lys Lys	Tyr Met Glu Leu Gly	Ile Ser Pro Thr Ile Lys
290	295	300
Lys Met Pro Gly	Gly Met Ile His Phe	Ser Gly Phe Asp Asn Asp
305	310	315
Arg Ala Asp Gln	Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu
320	325	330
Ser Asn Asp Leu	Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser
335	340	345
Thr Gly Ser Gly	Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys
350	355	360
Asn Trp Lys Arg	Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp
365	370	375
Val Asp Val His	Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg
380	385	390
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly
395	400	405
Asn Asp Ala Asn	Cys Ala Tyr Gly	
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcattctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
catcgttccc gtgaatccag aggc 24

<210> 299
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gaagggaggc cttcctttca gtggaccocgg gtcaagaata cccac 45

<210> 300
<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtagca 50
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
gcccatggag tgaatgctca cgcacctgcg ggggaggggc ctctactct 300
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400
ctcagcaatg ctacgtcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550
atggtacgag ttgctataca gaatctttgg atatgtgcat cagtggttta 600
tgccaaattg ttggctgaga tcaccagctg ggaagcaccg tcaaggaaga 650
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700
ggcagtataa atcccagctc tccgcaacca aatcgatga tactgtggtt 750
gcatttcct atggaagtag acatattcgc cttgtcttaa aaggtcctga 800
tcatttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttggtg acaattctag tgtggacttc 900

cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
 agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000
 agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050
 tttccttgct cagcaacctg tggaggaggt tatcagctga catcggtga 1100
 gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150
 attacccaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg 1200
 gatccttgct cagccagtga cggatacaag cagatcatgc cttatgacct 1250
 ctaccatccc cttcctcggg gggaggccac cccatggacc gcgtgctcct 1300
 cctcgtgtgg ggggggcatc cagagccggg cagtttctctg tgtggaggag 1350
 gacatccagg ggcatgtcac ttcagtggaa gagtggaaat gcatgtacac 1400
 ccctaagatg cccatcgcgc agccctgcaa catttttgac tgcctaaat 1450
 ggctggcaca ggagtggctt ccgtgcacag tgacatgtgg ccagggcctc 1500
 agataccgtg tggctcctctg catcgaccat cgaggaatgc acacaggagg 1550
 ctgtagccca aaaacaaagc cccacataaa agaggaatgc atcgtacca 1600
 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650
 tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700
 gccctcgtaa gttgtaaaag cacagactgt tctatatattg aaactgtttt 1750
 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
 taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850
 ttagtttcaa aaaaaaaaaa 1869

<210> 301
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 301
 Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe
 1 5 10 15
 Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu
 20 25 30
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys
 35 40 45
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
 50 55 60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr	
				65					70					75	
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala	
				80					85					90	
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe	
				95					100					105	
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser	
				110					115					120	
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala	
				125					130					135	
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp	
				140					145					150	
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln	
				155					160					165	
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly	
				170					175					180	
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	
				185					190					195	
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr	
				200					205					210	
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	
				215					220					225	
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser	
				230					235					240	
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	
				245					250					255	
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	
				260					265					270	
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala	
				275					280					285	
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg	
				290					295					300	
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly	
				305					310					315	
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn	
				320					325					330	
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile	
				335					340					345	
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro	

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggccc 50
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctggggcggg cgctgtggct ggcggcccg cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag gcggcgggtc agctccgccc cgagctccgc caggccgcgg 350
 agtgcgccc agagcctggc gtcagcgggg tgggcgagct catagtccg 400
 gagctggacc tcgcctcgct gcgctcgggt cgcgcttct gccaggaaat 450

gctccaggaa gaggctaggc tggatgtctt gatcaataac gcagggatct 500
 tccagtgcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
 gtgaaccatc tggggcactt tctactcacc aatctttctcc ttggactcct 600
 caaaagttca gctcccagca ggattgtggt agttttcttcc aaactttata 650
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaaactg gctaacattc tttttaccag 750
 ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900
 agtagaaggt gccagactt ccattttattt ggctcttca cctgaggtag 950
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
 agtgatggtt ggcttgctaa aataggaaca aggagtaaaa gagctgttta 1100
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtatttttg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400
 agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
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Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20					25					30	

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35				40					45	

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	
				50					55					60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	
				65					70					75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	
				80					85					90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	
				95					100					105	
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	
				110					115					120	
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	
				125					130					135	
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	
				140					145					150	
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	
				155					160					165	
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	
				170					175					180	
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	
				185					190					195	
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	
				200					205					210	
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	
				215					220					225	
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	
				230					235					240	
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	
				245					250					255	
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	
				260					265					270	
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	
				275					280					285	
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	
				290					295					300	
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	
				305					310					315	
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	
				320					325					330	
Met	Val	Gly	Leu	Leu	Lys										

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 34, 62, 87, 221, 229
 <223> unknown base

<400> 304
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
 gcaagaaaat tntgggatat cagtgaagtg atgggtngcc tgctaaaata 100
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
 tttcatggcc aaagtgttaa ctagtgttac tacaatgttt ggtgtttgtg 500
 tggaaattat ctgcctggct t 521

<210> 305
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 305
 ccaggaaatg ctccaggaag agcc 24

<210> 306
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 306
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308
<211> 1523
<212> DNA
<213> Homo sapiens

<400> 308
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100
ccagcgctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggttaactt 200
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaacia tgctgatgtt gcttttagtaa atttttatgc 300
tgactgggtg cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850
gataaatgtg ttctcttctg ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
 ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150
 ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200
 actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250
 gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 309
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser
 1 5 10 15
 Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu
 20 25 30
 Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn
 35 40 45
 Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe
 50 55 60
 Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile
 65 70 75
 Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val
 80 85 90
 Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser
 95 100 105
 Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys
 110 115 120
 Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr
 125 130 135
 Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu
 140 145 150
 Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly
 155 160 165

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 36, 48
<223> unknown base

<400> 310
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
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cggagcccag ccttttcta acccaaccca acctagccn gtcccagccg 150
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttaccgacc tcagatgctc ccttctgctc ctggtaactt 250
gggtttttac tctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactgggtg cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
tgagaggcct ctctggaagt tg 22

<210> 313
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 313
 gtcagcgatc agtgaaagc 19

 <210> 314
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 <220>
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 <400> 314
 ccagaatgaa gtagctcggc 20

 <210> 315
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 <400> 315
 ccgactcaaa atgcattgtc 20

 <210> 316
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 316
 catttggcag gaattgtcc 19

 <210> 317
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 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 317
 ggtgctatag gccaaagg 18

 <210> 318
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttacccg acctcagatg ctcccttctg ctctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

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gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatggt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggg ccagttaagt gcatgcaaaa agccacaaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttccacat 600
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 ttctaactcg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
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 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

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Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25					30
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40					45
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55					60
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70					75
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85					90
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100					105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323
<211> 477
<212> DNA
<213> Homo sapiens

<400> 323
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tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttgggtccagt taagtgcag caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgac agttacttta aaaaatg 477

<210> 324
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 325
caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

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ggaccaact ggggctcccg ccgctgctgc tgctgacat ggccttggcc 150
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctaccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttoccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
ggtatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
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ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
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ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100
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caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

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Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr	35	40	45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr	50	55	60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg	65	70	75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn	80	85	90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser	95	100	105	
Gln	Ser	Asp	Glu	Gln	Tyr	Ala	Cys	His	Leu	Gly	Cys	Gln	Asn	Gln	110	115	120	

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

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ggctgttttc aatttgtag tttgtggatg atggaattga cttaaactga 150
actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaattctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgtg 250

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aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
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<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
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cgaaggaggc ctttgggtga ggaccaact ggggctcccgc ccgctgctgc 150
tgctgaccat ggccttggcc ggagggtcgg ggaccgcttc ggctgaagca 200
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
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tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 334
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattcttggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
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<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
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agggcgccacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccc cggtctggga ttcttggttg 200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1885

<210> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
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Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25						30
Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp
			35						40					45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg
			50					55						60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg
			65					70						75

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	
				80					85					90	
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	
				95					100					105	
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	
				110					115					120	
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	
				125					130					135	
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	
				140					145					150	
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	
				155					160					165	
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	
				170					175					180	
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	
				185					190					195	
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	
				200					205					210	
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	
				215					220					225	
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	
				230					235					240	
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	
				245					250					255	
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	
				260					265					270	
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	
				275					280					285	
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	
				290					295					300	
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	
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Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	
				320					325					330	
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	
				335					340					345	
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	
				350					355					360	
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	

365	370	375
Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp		
380	385	390
Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr		
395	400	405
Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu		
410	415	420
Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu		
425	430	435
Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile		
440	445	450
Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln		
455	460	465

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct tttaacagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
 acttcatgaa atcaagtcac ttcttttgca ttttgatgag aattcatttt 500
 tttgctg 507

<210> 339
 <211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
aagctgccgg agctgcaatg 20

<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgcttctta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac tttcgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 343
tgtccagaaa caggcacata tcagc 25

<210> 344
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggaag cgtgggttgg gagggggcag 50

gatggggagg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggactttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg cctgttaggg ggggcccaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agagggtggt ggcagtgtct ctgaaggtcc ataaaagaaa 550

aaagagaagt gtggttaaggg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggagg tagtcttcac 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatatt ccccatcccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgcccgtg tggatgcttc 800

attccagcct cagggaagcc tggcaccac tgccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900

gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc taccctcatt 950

gctacctaat gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000

cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050

caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100

catggtgaaa ctccatctct actaaaaaaa aaaaaatata aaaattagct 1150

ggggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
 ggagactctc acttcaaccc aggaggtgga gggtgcggtg agccaagatt 1250
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 346
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
 1 5 10 15
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
 20 25 30
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
 35 40 45
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
 50 55 60
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
 65 70 75
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
 80 85 90
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
 95 100 105
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
 110 115 120
 Phe Met Val Ser

<210> 347
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 22
 <223> unknown base

<400> 347

cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
 ggagaggggac agaggccaga ggacttctca tactggacag aaaccgatca 150
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttct 200
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
 gggggtggac agcgatggat gctgggtggg gcccccctggg atgggccttc 350
 aggcgaccgg agggggggacg tttatcgctg ccctgtaggg gggggccaca 400
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
 tggtgatgg 509

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

agggacagag gccagaggac ttc 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

caggtgcata ttcacagcag gatg 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

ggaactcccc ttcgtcactc acctgttctt gcccttggtg ttcct 45

<210> 351

<211> 2056

<212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggaggggtgct tggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
ccccagcagc tgggtgctc acactgaagg tctgagtgat gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagcc tgggtgccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca tccccctggt 950
actggccctg tttgcctttg ttggcttcat gctgacctt gtggtcgtgc 1000
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
gtgggtggtcc tcccagacac cttgaaaata accaattcac ccagaagtt 1100
aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350
gtctaacaga aactgactg aggccttaggg gatgtgacct ctagactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcattccctt 1450
 cggctcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacacccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact gggaggcttg gagagcccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgtcctttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu
 1 5 10 15
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp
 20 25 30
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 35 40 45
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro
 50 55 60
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu
 65 70 75
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser
 80 85 90
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
 95 100 105
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln
 110 115 120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	125	130	135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	140	145	150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	155	160	165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	170	175	180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	185	190	195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	200	205	210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	215	220	225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 353
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748, 827
 <223> unknown base

<400> 353
 tcctgctgat gcacatctgg gtttgccaaa aggaggttgc ttcgagccgc 50
 cctttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
 agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcaciaa tggttctaga agaaatctgg acaagtcttt 250
 tcatgtgggt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctgggt ctcaactcact gaaggctctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
 agaaactcaa ccatacttac ccgacctggg atggagatca ccaaagatgg 650
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
 ggcgctgggt tgat 864

<210> 354
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 354
 aggcttcgct gcgactagac ctc 23

<210> 355
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 355
 ccaggtcggg taaggatggt tgag 24

<210> 356
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357

<211> 1670

<212> DNA

<213> Homo sapiens

<400> 357

cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
tggagacctg gagttagggt gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
cgtctgagcg cccctcgagc gctgggtactc tgggctgcac tgggggcagc 650
agctcacatc ggaccagcac ctgacccga ggactgggtg agctacaagg 700
ataatctcca gggaaacttc gtgccagggc ctccctttctg gggcctgggtg 750
aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gcccgtgga 800
tgtggagctg aagagggttc tttatgacct ctttctgccc ccattaaggc 850
tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900
catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950
tcccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000
ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050
gctgaggtgc agctcattca cttcaaccag gaactctacg ggaatttcag 1100
cgctgcctcc cgcgccccca atggcctggc cattctcagc ctctttgtca 1150
acgttgccag tacctctaac ccattcctca gtgcctcct taaccgcgac 1200
accatcactc gcattctcta caagaatgat gcctactttc ttcaagacct 1250

gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300
 gctctctcag caccgccccc tgctccgaga ctgtcacctg gatcctcatt 1350
 gaccggggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400
 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450
 ggccccctgca gcccttggcc cacagggcac tgagggggcaa cagggacccc 1500
 cggcaccccc agaggcgctg ccgaggcccc aactaccgcc tgcattgtgga 1550
 tgggtgtcccc catggctcgt gagactcccc ttcgaggatt gcacccgccc 1600
 gtcctaagcc tccccacaag gcgaggggag ttaccacctaa aacaaaagcta 1650
 ttaaaggac agaatactta 1670

<210> 358
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 358
 Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu
 1 5 10 15
 Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp
 20 25 30
 Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe
 35 40 45
 Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser
 50 55 60
 Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu
 65 70 75
 Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser
 80 85 90
 Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg
 95 100 105
 His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser
 110 115 120
 Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu
 125 130 135
 Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn
 140 145 150
 His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln
 155 160 165
 Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn		
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile		
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu		
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser		
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile		
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg		
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser		
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg		
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro		
305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg		
320	325	

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

ggcgcctggg tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50

ccgccagcct ccgccgccga gctcgttcg tgtccccgcc cctcgctect 100

gcagctactg ctcaaaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag caccacgctc gccccggac gctcgggtgt caggcccttc 300

gcgagcgggg ctctccgtct gcggctccct gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggtcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtgga agagcctgtc ttggagattt tctgggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcattg ctagagcaat tccagccatg gtggttccca 550

atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggg 600

gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttgacc ttcataataa attacgaagt caggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850

ggcccccgac gtttcattga caatcgtggg atgatgaagt gaaagacttt 900

agctacccat atgaacatga atgcaaccca tattgtccat tcaggtgttc 950

tggccctgta tgtacacatt atacacaggt cgtgtgggca actagtaaca 1000

gaatcgggtg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050

atatggccca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100

ctggtggggc catgccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaaggg 1200
tcagacaggt attatccccc tcgagaagag gaaacaaatg aaatagaacg 1250
acagcagtca caagtccatg acacccatgt ccggacaaga tcagatgata 1300
gtagcagaaa tgaagtcata agcgcacagc aaatgtccca aattgtttct 1350
tgtgaagtaa gattaagaga tcagtgcataa ggaacaacct gcaataggta 1400
cgaatgtcct gctggctgtt tggatagtaa agctaaagtt attggcagtg 1450
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggg 1500
ataatagaca atgatgggtg ctgggtagat atcactagac aaggaagaaa 1550
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaaatt 1600
atcagtctgc taattccttc acagtctcta aagtaacagt tcaggctgtg 1650
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atattgccat atcatgggtac ctataatggg gatatatattg tttctatgaa 2900
aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950
at ttttttttc tgctgggtgga tttacatatt aaattttttc tgctgggtgga 3000
taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363
<211> 500
<212> PRT
<213> Homo sapiens

<400> 363
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Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr
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Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu
35 40 45
Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn
50 55 60
Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln
65 70 75
Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val
80 85 90
Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp
95 100 105
Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu
110 115 120
Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln
125 130 135
Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His
140 145 150
Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys
155 160 165
Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

170										175					180				
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile					
				185					190					195					
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly					
				200					205					210					
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser					
				215					220					225					
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys					
				230					235					240					
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu					
				245					250					255					
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His					
				260					265					270					
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser					
				275					280					285					
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg					
				290					295					300					
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala					
				305					310					315					
Gly	Cys	Leu	Asp	Ser	Lys	Ala	Lys	Val	Ile	Gly	Ser	Val	His	Tyr					
				320					325					330					
Glu	Met	Gln	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly	Ile					
				335					340					345					
Ile	Asp	Asn	Asp	Gly	Gly	Trp	Val	Asp	Ile	Thr	Arg	Gln	Gly	Arg					
				350					355					360					
Lys	His	Tyr	Phe	Ile	Lys	Ser	Asn	Arg	Asn	Gly	Ile	Gln	Thr	Ile					
				365					370					375					
Gly	Lys	Tyr	Gln	Ser	Ala	Asn	Ser	Phe	Thr	Val	Ser	Lys	Val	Thr					
				380					385					390					
Val	Gln	Ala	Val	Thr	Cys	Glu	Thr	Thr	Val	Glu	Gln	Leu	Cys	Pro					
				395					400					405					
Phe	His	Lys	Pro	Ala	Ser	His	Cys	Pro	Arg	Val	Tyr	Cys	Pro	Arg					
				410					415					420					
Asn	Cys	Met	Gln	Ala	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Gly	Thr					
				425					430					435					
Arg	Val	Tyr	Ser	Asp	Leu	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Val	His					
				440					445					450					
Ala	Gly	Val	Val	Arg	Asn	His	Gly	Gly	Tyr	Val	Asp	Val	Met	Pro					
				455					460					465					

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile
470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg
485 490 495

Val Phe Ala Val Val
500

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365

ccaagagtat actgtcctcg 20

<210> 366

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 366

agcacagatt ttctctacag ccccc 25

<210> 367

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

aaccactcca gcatgtactg ctgc 24

<210> 368

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100

agagaaagcc gagcagagct ggggtggcgtc tccggggccg cgctccgacg 150

ggccagcgcc ctcccctatgt ccctgctccc acgcccgcgc cctccgggtca 200

gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccagggtac 400

cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450

catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500

agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550

gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650

attgttatga agcacttttt accaacgggtc agtttttaca ttttatagct 700

gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750

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ctttataagc gcccgaggagg aacaatgagc ttggtggaca catttcattg 900

cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950

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<210> 370
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 370
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 20 25 30
 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys
 35 40 45
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 50 55 60
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val
 65 70 75
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln
 80 85 90
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys
 95 100 105
 Arg Arg Val Tyr Glu Glu
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<210> 371
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

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<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

tgcatgacat gctgcccata tggtttaccg ccaatttgga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

gccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tggatgaagac gaagatatcc atgatcagaa cagtaagaag 550

cccgtcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600

catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650

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 tgaagaaaga gtcaatgaga ttttgcccag cacatggagc tgtaatccag 3000
 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050
 aatctgtacg gttctgtgca aagaggtggt ttgccagcct gaactatatt 3100
 taagagactt tgt 3113

<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
			20						25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
			35					40						45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala

50					55					60				
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser
				155					160					165
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu
				170					175					180
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly
				185					190					195
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly
				200					205					210
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu
				215					220					225
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly
				230					235					240
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly
				245					250					255
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser
				260					265					270
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu
				275					280					285
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile
				290					295					300
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met
				305					310					315
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln
				320					325					330
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile
				335					340					345

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635					640					645				
Asn	Pro	Lys	His	Ser	Lys	Asp	Pro	His	Lys	Thr	Gly	Pro	Glu	Asp
				650					655					660
Thr	Thr	Val	Leu	Ile	Glu	Thr	Lys	Arg	Asp	Tyr	Ser	Thr	Glu	Leu
				665					670					675
Ser	Val	Thr	Ile	Ala	Val	Gly	Ala	Ser	Leu	Leu	Phe	Leu	Asn	Ile
				680					685					690
Leu	Ala	Phe	Ala	Ala	Leu	Tyr	Tyr	Lys	Lys	Asp	Lys	Arg	Arg	His
				695					700					705
Glu	Thr	His	Arg	Arg	Pro	Ser	Pro	Gln	Arg	Asn	Thr	Thr	Asn	Asp
				710					715					720
Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
				800					805					810
His	Ser	Thr	Thr	Arg	Val									
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<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggaccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ctttcttctt 100

ttgttgggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttcctcactg tggaaatctga tgggcaatgc catggtgatg 250

accagtgata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg caggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcattgggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450

ggacaaatth gtggggctgg gaggatthgt agacacctac cccaatgagg 500

agaagcagca agagcgggta ttcccctaca tctcagccat ggtgaacaac 550

ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600

aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttcctggtga 650

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ctactacttc ggcacctcct ccactactgg ggatctctca gataatcatg 800

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<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	275	280	285
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro	290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe	305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val	320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys	335	340	345

Arg Phe Tyr

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 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 381
 ccttggtcg tggcagcagt gg 22

<210> 382
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 382
 cactctccag gctgcatgct cagg 24

<210> 383
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 383
 gtcaaagctt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384
 <211> 3150
 <212> DNA
 <213> Homo sapiens

<400> 384

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ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
tggggtctgg ctccagaattc ctgcagctgg tgaaaatctg ttttctagaa 200
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agcctcttcc gaaagcccct tgaactcctt gcctctttac ccaaatcacc 750
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cagaacggtc agctgctgag ggatatctat ctaaagaaac aaaaactcct 850
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<210> 385
 <211> 480
 <212> PRT
 <213> Homo sapiens

<400> 385

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Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	35	40	45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	50	55	60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	65	70	75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	80	85	90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	95	100	105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	110	115	120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	125	130	135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	140	145	150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	155	160	165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	170	175	180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	185	190	195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	200	205	210	

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	215	220	225
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	230	235	240
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	245	250	255
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	260	265	270
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	275	280	285
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	290	295	300
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	305	310	315
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	320	325	330
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	335	340	345
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	350	355	360
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	365	370	375
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	380	385	390
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	395	400	405
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	410	415	420
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	425	430	435
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	440	445	450
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	455	460	465
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
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<210> 387
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 387
ttccctatgc tctgtattgg catgg 25

<210> 388
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
<211> 3313
<212> DNA
<213> Homo sapiens

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gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
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cctcgagtct ccagctaact ctgaaacctc agacctcact ctgtacctgg 2450
tggtagcggg ggccgcgggc tctgctgtct tctggcctt cgtcatcttg 2500
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acgggggtgca ggctttctct cagacctatt cccacgaggt ttccctcacc 2650
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aaactctatc tca 3313

<210> 390
<211> 916
<212> PRT
<213> Homo sapiens
<400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln	20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

290										295				300			
Ile	Ser	Thr	Ile	Gly	Glu	Leu	Asp	His	Glu	Glu	Ser	Gly	Phe	Tyr			
				305					310					315			
Gln	Met	Glu	Val	Gln	Ala	Met	Asp	Asn	Ala	Gly	Tyr	Ser	Ala	Arg			
				320					325					330			
Ala	Lys	Val	Leu	Ile	Thr	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro			
				335					340					345			
Glu	Val	Val	Leu	Thr	Ser	Leu	Ala	Ser	Ser	Val	Pro	Glu	Asn	Ser			
				350					355					360			
Pro	Arg	Gly	Thr	Leu	Ile	Ala	Leu	Leu	Asn	Val	Asn	Asp	Gln	Asp			
				365					370					375			
Ser	Glu	Glu	Asn	Gly	Gln	Val	Ile	Cys	Phe	Ile	Gln	Gly	Asn	Leu			
				380					385					390			
Pro	Phe	Lys	Leu	Glu	Lys	Ser	Tyr	Gly	Asn	Tyr	Tyr	Ser	Leu	Val			
				395					400					405			
Thr	Asp	Ile	Val	Leu	Asp	Arg	Glu	Gln	Val	Pro	Ser	Tyr	Asn	Ile			
				410					415					420			
Thr	Val	Thr	Ala	Thr	Asp	Arg	Gly	Thr	Pro	Pro	Leu	Ser	Thr	Glu			
				425					430					435			
Thr	His	Ile	Ser	Leu	Asn	Val	Ala	Asp	Thr	Asn	Asp	Asn	Pro	Pro			
				440					445					450			
Val	Phe	Pro	Gln	Ala	Ser	Tyr	Ser	Ala	Tyr	Ile	Pro	Glu	Asn	Asn			
				455					460					465			
Pro	Arg	Gly	Val	Ser	Leu	Val	Ser	Val	Thr	Ala	His	Asp	Pro	Asp			
				470					475					480			
Cys	Glu	Glu	Asn	Ala	Gln	Ile	Thr	Tyr	Ser	Leu	Ala	Glu	Asn	Thr			
				485					490					495			
Ile	Gln	Gly	Ala	Ser	Leu	Ser	Ser	Tyr	Val	Ser	Ile	Asn	Ser	Asp			
				500					505					510			
Thr	Gly	Val	Leu	Tyr	Ala	Leu	Ser	Ser	Phe	Asp	Tyr	Glu	Gln	Phe			
				515					520					525			
Arg	Asp	Leu	Gln	Val	Lys	Val	Met	Ala	Arg	Asp	Asn	Gly	His	Pro			
				530					535					540			
Pro	Leu	Ser	Ser	Asn	Val	Ser	Leu	Ser	Leu	Phe	Val	Leu	Asp	Gln			
				545					550					555			
Asn	Asp	Asn	Ala	Pro	Glu	Ile	Leu	Tyr	Pro	Ala	Leu	Pro	Thr	Asp			
				560					565					570			
Gly	Ser	Thr	Gly	Val	Glu	Leu	Ala	Pro	Arg	Ser	Ala	Glu	Pro	Gly			
				575					580					585			

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

875

880

885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

ccaggttaaa aggctccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccttgatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttctctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
aggaggacaa ggtgctgggg ggtcatgagt gcccaaccca ttcgcagcct 300
tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350
tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400
acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450
caagaaatac ctgtggttca gtccatccca caccctgct acaacagcag 500
cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
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ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800
tggaggcccc ctggtgtgtg atggtgcact ccagggcatc acatcctggg 850
gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900
tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950
ctaggataag cactagatct cccttaataa actcacaact ctctgggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccattccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccggggcgg gctgagcgcc tcttgcggcc cggcctgcgc 50

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gccccgcgc gggccgcgc ccgcgcgcgc gccaggtga gcgctccgc 150

cgccgcgagg ccccgcccc gccgcgcgc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcattcctcc gccggccgc gctgcgagcg ccccgccagt ccgcgcgcgc 300

gccgcctcg cctgtgcgc cctgcgcgc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

gggcccgggc cgggcccgtag cggcgcgcc tggatgcgga cccggccgcg 450

gggagacggg cggccgcccc gaaacgactt tcagtcccc agcgcccccg 500

cccaaccct acgatgaaga gggcgtccgc tggaggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccagggt 600

gcctgcgtat gctacaatga gccaagggtg acgacaagct gccccagca 650

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tcttgacgg caaccgcac tcgcatgtgc cagctgccag cttccgtgcc 750

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tgatgcggct gccttcaact gcctggccct cctggagcag ctggacctca 850

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ggccgcctac acacgtgca cctggaccgc tgcggcctgc aggagctggg 950

cccggggctg ttccggggc tggctgccct gcagtacct tacctgcagg 1000

acaacgcgct gcaggcactg cctgatgaca ccttccgcga cctgggcaac 1050

ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccagcg 1100

cgccttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150
 gcgtggccca tgtgcacccg catgccttcc gtgaccttgg ccgcctcatg 1200
 acactctatc tgtttgccaa caatctatca gcgctgcccc ctgaggccct 1250
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aacccttggg 1300
 tgtgtgactg ccgggcacgc ccactctggg cctgggtgca gaagttccgc 1350
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggttgccg 1400
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 ctggggcttc ccaagtgtg ccagccagat gccgctgaca aggcctcagt 1550
 actggagcct ggaagaccag cttcggcagg caatgcgtg aagggaacgcg 1600
 tgccgccccg tgacagcccc ccgggcaacg gctctggccc acggcacatc 1650
 aatgactcac cttttgggac tctgcctggc tctgctgagc ccccgctcac 1700
 tgcagtgcgg cccgagggct ccgagccacc aggggtcccc acctcgggcc 1750
 ctgcgccgag gccaggctgt tcacgcaaga accgcacccg cagccactgc 1800
 cgtctggggc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850
 ctcaggtgcc ctaccagcc tcacctgcag cctcaccccc ctgggectgg 1900
 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000
 ccgccaagcc agccgggcgg ccgaccctg gggcaggcca ggccaggtcc 2050
 tccctgatgg acgctgccc cccgccaccc ccactctcac cccatcatgt 2100
 ttacaggggt cggcggcagc gtttgttcca gaacgccgcc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20					25					30	

Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atattttctga ggtatctgta gaataaccac 100

agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gaggggaattc 350

tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400

gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ctttcgagtt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600

cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650

ttagatgtag gccaaaacaa tattgagaac tatataatca gcccgaactc 700

ctattttcgg gtcttcaccc gcaaacgcag tgatggcagg aaataccag 750

agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800

ttaacactca cagcactgga tgggtggctct ccgcccagat ctggcactgc 850

tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900

agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950

ctggttgtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000

gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050

agatcaatcc cttgacagga gaaattgaac taaaaaaaca actcgatttc 1100

gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

cttttctgga aaatgcaccg ttctgattca agtgatagat gtgaacgacc 1200
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 gcgcctgaaa ctgtggttgc acttttccagt gtttcagatc ttgattcagg 1300
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 tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400
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 gtgcctggg aaagaaatac aaggaaattc taccttcccc aataactttg 2550
 ggttcaatat tcagtacca tagttgactt ttacattcca taggtatttt 2600

atattgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650
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 tgttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu	1	5	10	15
Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu	20	25	30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe	35	40	45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe	50	55	60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His	65	70	75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys	80	85	90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu	95	100	105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala	110	115	120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu	125	130	135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly	140	145	150	
Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln	155	160	165	
Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg	170	175	180	
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	185	190	195	
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg	200	205	210	
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	215	220	225	
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala				

230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp		
245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val		
260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala		
275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly		
290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser		
305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly		
320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala		
335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn		
350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp		
365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu		
380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr		
395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr		
410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu		
425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala		
440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser		
455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser		
470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp		
485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn		
500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln		
515	520	525

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	530	535	540
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	545	550	555
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	560	565	570
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	575	580	585
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	590	595	600
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	605	610	615
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	620	625	630
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	635	640	645
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	650	655	660
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	665	670	675
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	680	685	690
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	695	700	705
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	710	715	720
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	725	730	735
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	740	745	750
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	755	760	765
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	770	775	780
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	785	790	795

Asn Ile Gln

<210> 406

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
ctgagaacgc gcctgaaact gtg 23

<210> 407
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
agcgttgctca ttgacatcgg cg 22

<210> 408
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409
<211> 1379
<212> DNA
<213> Homo sapiens

<400> 409
accacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50
gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
cggtcgacga ccgcccgcg tcatgcggct cctcggctgg tggcaagtat 150
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250
ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atgggccagg 300
acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500

cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550
 atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
 actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700
 aaacggtagt gactgtactc tagtcctggt ttacaccccg tggtgccgct 750
 tttctgccag tttggcccct cactttaact ctctgccccg ggcatttcca 800
 gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850
 caggtttggc accgtagctg ttcctaataat tttattattt caaggagcta 900
 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
 atcttcattt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000
 aactcaagcc gaccaaataag gccctcttcc cagcactttg ataaaaagtg 1050
 tggactgggt gcttgtattt tccttattct ttttaattag ttttattatg 1100
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 gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaaac 1200
 ttcaatcctt cgtttcagaa attagtgcta cagtttcata cattttctcc 1250
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350
 caataagcaa atgcaaaaat attcaatag 1379

<210> 410
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu
 1 5 10 15
 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val
 20 25 30
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu
 35 40 45
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
 50 55 60
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala
 65 70 75
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
				140					145					150					
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
				155					160					165					
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411

<211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 411
 cacagagcca gaagtggcgg aatc 24

 <210> 412
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 412
 ccacatgttc ctgctcttgc cctgg 25

 <210> 413
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 413
 cggtagtgc tgtactctag tctgtttta cccccgtgg tgccg 45

 <210> 414
 <211> 1196
 <212> DNA
 <213> Homo sapiens

 <400> 414
 cccggctccg ctccctctgc cccctcgggg tcgcgcgccc acgatgctgc 50
 agggccctgg ctgcgtctgc ctgctcttcc tcgcctcgca ctgctgcctg 100
 ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150
 gcgcagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200
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 aaggaggtgc tggagcaggc cggcgcttgg atcccgtgg tcatgaagca 300
 gtgccacccg gacaccaaga agttcctgtg ctgcgtcttc gccccgtct 350
 gcctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400
 caggtgaagg accgctgcgc cccggtcatg tccgccttcg gcttcccctg 450
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gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800
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agcttcccc tgcttttgc acgtttgcat cccagcatt tctgagtta 1100
taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccacc 1150
gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415
<211> 295
<212> PRT
<213> Homo sapiens

<400> 415

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser	1	5	10	15
His	Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln	20	25	30	
Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val	35	40	45	
Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu	50	55	60	
Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln	65	70	75	
Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp	80	85	90	
Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp	95	100	105	
Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln	110	115	120	
Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro	125	130	135	

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	140	145	150
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	155	160	165
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	170	175	180
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	185	190	195
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	200	205	210
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	215	220	225
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	230	235	240
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	245	250	255
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	260	265	270
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	275	280	285
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						290	295	

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

cctggctcgc tgctgctgct c 21

<210> 417

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

cctcacaggt gcactgcaag ctgtc 25

<210> 418

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acgggggttg 50

ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtccat ggagcagatc aactggctgt cactgggtcta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagacc tggatcatctt 450

ctctccagcc aagctggctg ccttgtgggt cccagagcac cagcgagcca 500

cggccaacat gctcgcacc atgtcgaacc ctctgggcgt ccttgtggcc 550

aatgtgtgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600

gctcgggtgc tataccatcc ctgctggcgt cgtctgcctg ctgtccacca 650

tctgcctgtg ggagagtgtg cccccaccc cgcctctgc cggggctgcc 700

agctccacct cagagaagtt cctggatggg ctcaagctgc agctcatgtg 750

gaacaaggcc tatgtcatcc tggtgtgtg cttgggggga atgatcgga 800

tctctgccag cttctcagcc ctctggagc agatcctctg tgcaagcggc 850

cactccagtg ggttttcgg cctctgtggc gctctcttca tcacgtttgg 900

gatcctgggg gcaactggctc tcggccccta tgtggaccgg accaagcact 950

tcactgaggc caccaagatt ggctgtgcc tgttctctct ggctgcgtg 1000

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 cccggctggg tctcactcct ccttctcctc cccgtgggtg atcacgtagc 1700
 tgagcgcctt gtagtcagg ttgcccgcga catcgatgga ggcgaactgg 1750
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<210> 420
 <211> 560
 <212> PRT
 <213> Homo sapiens

<400> 420
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 Val Phe Leu Leu Ala Ile Ser Leu Leu Asn Cys Ser Asn Ala Thr
 35 40 45
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp
 50 55 60
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr
 65 70 75
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu
 80 85 90
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu
 95 100 105
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val

	110		115		120
Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu	125		130		135
Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu	140		145		150
Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met	155		160		165
Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val	170		175		180
Leu Ser Pro Val Leu Val Lys Lys Gly Glu Asp Ile Pro Leu Met	185		190		195
Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser	200		205		210
Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala	215		220		225
Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys	230		235		240
Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys	245		250		255
Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu	260		265		270
Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly	275		280		285
Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu	290		295		300
Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala	305		310		315
Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe	320		325		330
Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala	335		340		345
Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val	350		355		360
Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly	365		370		375
Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile	380		385		390
Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu	395		400		405

Pro	Ser	Leu	Ser	Thr	Cys	Gln	Gln	Gly	Glu	Asp	Pro	Leu	Asp	Trp	410	415	420
Thr	Val	Ser	Leu	Leu	Leu	Met	Ala	Gly	Leu	Cys	Thr	Phe	Phe	Ser	425	430	435
Cys	Ile	Leu	Ala	Val	Phe	Phe	His	Thr	Pro	Tyr	Arg	Arg	Leu	Gln	440	445	450
Ala	Glu	Ser	Gly	Glu	Pro	Pro	Ser	Thr	Arg	Asn	Ala	Val	Gly	Gly	455	460	465
Ala	Asp	Ser	Gly	Pro	Gly	Val	Asp	Arg	Gly	Gly	Ala	Gly	Arg	Ala	470	475	480
Gly	Val	Leu	Gly	Pro	Ser	Thr	Ala	Thr	Pro	Glu	Cys	Thr	Ala	Arg	485	490	495
Gly	Ala	Ser	Leu	Glu	Asp	Pro	Arg	Gly	Pro	Gly	Ser	Pro	His	Pro	500	505	510
Ala	Cys	His	Arg	Ala	Thr	Pro	Arg	Ala	Gln	Gly	Pro	Ala	Ala	Thr	515	520	525
Asp	Ala	Pro	Ser	Arg	Pro	Gly	Arg	Leu	Ala	Gly	Arg	Val	Gln	Ala	530	535	540
Ser	Arg	Phe	Ile	Asp	Pro	Ala	Gly	Ser	His	Ser	Ser	Phe	Ser	Ser	545	550	555
Pro	Trp	Val	Ile	Thr											560		

<210> 421
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 421
 agcttctcag ccctcctgga gcag 24

<210> 422
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 422
 cgggtcaata aacctggacg cttgg 25

<210> 423
 <211> 43
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtccacatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50

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tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150

tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300

tctgaatcta gccacttg cggtaagcat gatgcaactt ctgcaacttc 350

tgctggggct tttggggcca ggtggctact tatttctttt aggggattgt 400

caggaggtga ccactctcac ggtgaaatac caagtgtcag aggaagtgcc 450

atctggtaca gtgatcggga agctgtccca ggaactgggc cgggaggaga 500

ggcggaggca agctggggcc gccttcaggt tgttgacagct gcctcaggcg 550

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gtgctggaca tcaatgacca ccagccacgg tttcccaaag gcgagcagga 750

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gagctcttga ccagacaca ggcctaaca ccctgcacac ctacactctg 850

tctcccagtg agcactttgc cttggatgtc attgtgggcc ctgatgagac 900

caaacatgca gaactcatag tggatgaagga gctggacagg gaaatccatt 950

cattttttga tctggtgtta actgcctatg acaatgggaa ccccccaag 1000

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 aaaaaaaaaa aaa 4313

<210> 425
 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 425
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 Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu
 20 25 30
 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val
 35 40 45
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg
 50 55 60
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu
 65 70 75
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg
 80 85 90
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu
 95 100 105
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His
 110 115 120
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe
 125 130 135
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu
 140 145 150
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly
 155 160 165
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe
 170 175 180
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu
 185 190 195

Leu	Ile	Val	Val	Lys	Glu	Leu	Asp	Arg	Glu	Ile	His	Ser	Phe	Phe	200	205	210
Asp	Leu	Val	Leu	Thr	Ala	Tyr	Asp	Asn	Gly	Asn	Pro	Pro	Lys	Ser	215	220	225
Gly	Thr	Ser	Leu	Val	Lys	Val	Asn	Val	Leu	Asp	Ser	Asn	Asp	Asn	230	235	240
Ser	Pro	Ala	Phe	Ala	Glu	Ser	Ser	Leu	Ala	Leu	Glu	Ile	Gln	Glu	245	250	255
Asp	Ala	Ala	Pro	Gly	Thr	Leu	Leu	Ile	Lys	Leu	Thr	Ala	Thr	Asp	260	265	270
Pro	Asp	Gln	Gly	Pro	Asn	Gly	Glu	Val	Glu	Phe	Phe	Leu	Ser	Lys	275	280	285
His	Met	Pro	Pro	Glu	Val	Leu	Asp	Thr	Phe	Ser	Ile	Asp	Ala	Lys	290	295	300
Thr	Gly	Gln	Val	Ile	Leu	Arg	Arg	Pro	Leu	Asp	Tyr	Glu	Lys	Asn	305	310	315
Pro	Ala	Tyr	Glu	Val	Asp	Val	Gln	Ala	Arg	Asp	Leu	Gly	Pro	Asn	320	325	330
Pro	Ile	Pro	Ala	His	Cys	Lys	Val	Leu	Ile	Lys	Val	Leu	Asp	Val	335	340	345
Asn	Asp	Asn	Ile	Pro	Ser	Ile	His	Val	Thr	Trp	Ala	Ser	Gln	Pro	350	355	360
Ser	Leu	Val	Ser	Glu	Ala	Leu	Pro	Lys	Asp	Ser	Phe	Ile	Ala	Leu	365	370	375
Val	Met	Ala	Asp	Asp	Leu	Asp	Ser	Gly	His	Asn	Gly	Leu	Val	His	380	385	390
Cys	Trp	Leu	Ser	Gln	Glu	Leu	Gly	His	Phe	Arg	Leu	Lys	Arg	Thr	395	400	405
Asn	Gly	Asn	Thr	Tyr	Met	Leu	Leu	Thr	Asn	Ala	Thr	Leu	Asp	Arg	410	415	420
Glu	Gln	Trp	Pro	Lys	Tyr	Thr	Leu	Thr	Leu	Leu	Ala	Gln	Asp	Gln	425	430	435
Gly	Leu	Gln	Pro	Leu	Ser	Ala	Lys	Lys	Gln	Leu	Ser	Ile	Gln	Ile	440	445	450
Ser	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Val	Phe	Glu	Lys	Ser	Arg	Tyr	455	460	465
Glu	Val	Ser	Thr	Arg	Glu	Asn	Asn	Leu	Pro	Ser	Leu	His	Leu	Ile	470	475	480
Thr	Ile	Lys	Ala	His	Asp	Ala	Asp	Leu	Gly	Ile	Asn	Gly	Lys	Val			

485	490	495
Ser Tyr Arg Ile Gln Asp Ser Pro Val	Ala His Leu Val Ala	Ile
500	505	510
Asp Ser Asn Thr Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr	
515	520	525
Glu Glu Met Ala Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser	
530	535	540
Gly Gln Pro Met Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu	
545	550	555
Leu Asp Ala Asn Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu	
560	565	570
Ser Asp Gly Lys Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr	
575	580	585
Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	
590	595	600
Ala Gly Thr Asp Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	
605	610	615
Phe Leu Leu Thr Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	
620	625	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	
635	640	645
Leu Phe Ile Leu Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val	
650	655	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile	
665	670	675
Val Val Glu Asp Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	
680	685	690
Leu Arg Val Met Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser	
695	700	705
Ala Arg Lys Pro Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile	
710	715	720
Cys Leu Ala Val Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	
725	730	735
Phe Met Ser Ile Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	
740	745	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	
755	760	765
Pro Gln Lys His Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val	
770	775	780

Leu Arg Gly Gln	Ala Gly Glu Pro Cys	Glu Val Gly Gln Ser His
785	790	795
Lys Asp Val Asp	Lys Glu Ala Met Met	Glu Ala Gly Trp Asp Pro
800	805	810
Cys Leu Gln Ala	Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg Thr
815	820	825
Leu Arg Asn Gln	Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg Glu
830	835	840
Val Leu Gln Asp	Thr Val Asn Leu Leu	Phe Asn His Pro Arg Gln
845	850	855
Arg Asn Ala Ser	Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln Pro
860	865	870
Ala Thr Gly Gln	Pro Arg Ser Arg Pro	Leu Lys Val Ala Gly Ser
875	880	885
Pro Thr Gly Arg	Leu Ala Gly Asp Gln	Gly Ser Glu Glu Ala Pro
890	895	900
Gln Arg Pro Pro	Ala Ser Ser Ala Thr	Leu Arg Arg Gln Arg His
905	910	915
Leu Asn Gly Lys	Val Ser Pro Glu Lys	Glu Ser Gly Pro Arg Gln
920	925	930
Ile Leu Arg Ser	Leu Val Arg Leu Ser	Val Ala Ala Phe Ala Glu
935	940	945
Arg Asn Pro Val	Glu Glu Leu Thr Val	Asp Ser Pro Pro Val Gln
950	955	960
Gln Ile Ser Gln	Leu Leu Ser Leu Leu	His Gln Gly Gln Phe Gln
965	970	975
Pro Lys Pro Asn	His Arg Gly Asn Lys	Tyr Leu Ala Lys Pro Gly
980	985	990
Gly Ser Arg Ser	Ala Ile Pro Asp Thr	Asp Gly Pro Ser Ala Arg
995	1000	1005
Ala Gly Gly Gln	Thr Asp Pro Glu Gln	Glu Glu Gly Pro Leu Asp
1010	1015	1020
Pro Glu Glu Asp	Leu Ser Val Lys Gln	Leu Leu Glu Glu Glu Leu
1025	1030	1035
Ser Ser Leu Leu	Asp Pro Ser Thr Gly	Leu Ala Leu Asp Arg Leu
1040	1045	1050
Ser Ala Pro Asp	Pro Ala Trp Met Ala	Arg Leu Ser Leu Pro Leu
1055	1060	1065
Thr Thr Asn Tyr	Arg Asp Asn Val Ile	Ser Pro Asp Ala Ala Ala

1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
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Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 427
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 427
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<210> 428
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 428
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<210> 429
 <211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 430

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			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
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Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln	185	190	195
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala	200	205	210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser	215	220	225
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly	230	235	240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu	245	250	255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala	260	265	270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr	275	280	285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys	290	295	300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys	305	310	315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu	320	325	330
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe	335	340	345
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu	350	355	360
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser	365	370	375
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr	380	385	390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu	395	400	405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn			

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu		
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440	445	450
Lys Gln Met Ala Pro		
455		

<210> 431
 <211> 407
 <212> DNA
 <213> Homo sapiens

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 <222> 78, 81, 113, 157, 224, 297
 <223> unknown base

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 tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
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 tttccag 407

<210> 432
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
 <223> unknown base

<400> 432
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 ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
 ttgaatagca gctcccgta ttttactgg aaaatgaacc tgtgtgtaat 300
 tctgctgac ctggttttca tggcgcttt ttacattggc tattttattg 350
 tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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 cattctc 457

<210> 433
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
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<210> 434
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
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<210> 435
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 435
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<210> 436
 <211> 3951
 <212> DNA
 <213> Homo sapiens

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 ttctcacggg ctgctgcctt caatctggac gtgatgggtg ccttgcgcaa 150
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a 3951

<210> 437
 <211> 1141
 <212> PRT
 <213> Homo sapiens

<400> 437

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Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
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Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
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Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
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Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly

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Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
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Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
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Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
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Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
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Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
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Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
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Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
				185					190					195					
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
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Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
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Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
				230					235					240					
Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
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Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
				260					265					270					
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
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Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
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Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
				305					310					315					
Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
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Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
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Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
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Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala	
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Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val	
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Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly	
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Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly	
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Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser	
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Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser	
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Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His	
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Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu	
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Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg	
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Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys	
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Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp	

665					670					675				
Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser	Gly	Gln	Pro	Val	Ile	Gly
				680					685					690
Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro
				695					700					705
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met
				710					715					720
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro
				725					730					735
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val
				740					745					750
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr
				755					760					765
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr
				770					775					780
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu
				785					790					795
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro
				800					805					810
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser
				815					820					825
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val
				830					835					840
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln
				845					850					855
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro
				860					865					870
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val
				875					880					885
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser
				890					895					900
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg
				905					910					915
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu
				920					925					930
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu
				935					940					945
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn
				950					955					960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala
 965 970 975
 Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu
 980 985 990
 Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn
 995 1000 1005
 Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala
 1010 1015 1020
 Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val
 1025 1030 1035
 Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu
 1040 1045 1050
 Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys
 1055 1060 1065
 Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro
 1070 1075 1080
 Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe
 1085 1090 1095
 Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser
 1100 1105 1110
 Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp
 1115 1120 1125
 Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr
 1130 1135 1140
 Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 441
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agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100
ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200
ccgcgccggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
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aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tggttaagaga gcatgcagtg acctggagtt 750
caggggaagtg gcaaacagat tgccgggactg gttcaaggcc cttcatgaaa 800
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
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gtttaacaga cttgatataa actatgacct gctattggac cagtcagagc 950

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 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250
 gaataaatgg tgttgcatg tgtgctatag attttgagat ctccggagat 1300
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 gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450
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 cctatttaaa attatcttct tccccaataa caaatgatt ctaaacctca 1550
 catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600
 ttatgtttta ataagaatca tttgctttga gtttttatat tccttacaca 1650
 aaaagaaaat acatatgcag tctagtcaga caaataaag ttttgaagtg 1700
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 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442
 <211> 436
 <212> PRT
 <213> Homo sapiens

<400> 442
 Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp
 1 5 10 15
 Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly
 20 25 30
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu
 35 40 45
 Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

50										55					60				
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					
				320					325					330					
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly					
				335					340					345					

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
				425					430					435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatgggc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gagcggagac aacagtaoct gacgcctctt tcagcccggg atcgccccag 100
cagggatggg cgacaagatc tggctgcctt tccccgtgct ccttctggcc 150
gctctgcctc cgggtgctgt gcctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaocttta cccttccgc cggccagaag gagtgttct 250
accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400
ctgaagttgg tgattacatg ttctgcttg acaatacatt cagcaccatt 450
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatgggttaa tttagtggc atgggtggg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850
tgttacagtc aagaccatta atgggtcttct ccaaaatatt ttgagatata 900
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950
tgtgcaagta atcctgctga tccagttgta ctttaagtgtg taacaggaat 1000
attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050
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 agaatttaga aaaacttgag aaaacctaata ccaaaataaa attcacttaa 1850
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 tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950
 aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000
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 gtgaaatttt aaaagacatt gattccgcac gtaaggattt ttcacttgaa 3500
 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu		
125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp		
140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser		
155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe		
170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val		
185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser		
200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg		
215	220	225
Lys Ser Arg Thr		

<210> 448
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
 cccagcaggg ctgggcgaca aga 23

<210> 449
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 gtcttccagt ttcatatcca ata 23

<210> 450
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
 ccagaaggag cacggggaag ggcagccaga tcttgcgcc cat 43

<210> 451
 <211> 859
 <212> DNA
 <213> Homo sapiens

<400> 451
 ccacccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50
 agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100
 gccctgcccc gtgtgtcctg gatgctgctt tcctgacctca ttctcctgtg 150
 tcagggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
 gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttggtt 250
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
 ctctggaaaa ctggtgtctg tgctcagtg ggctgaggga tccttcgtgt 350
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 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
 ccactttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550
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 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700
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 gagatctcag agaataataa taaaatggt actttataaa aaaaaaaaaa 850
 aaaaaaaaaa 859

<210> 452
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 452
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 1 5 10 15
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln
 20 25 30
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys
 35 40 45
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

50	55	60
Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys		
65	70	75
Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser		
80	85	90
Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly		
95	100	105
Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp		
110	115	120
Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys		
125	130	135
Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser		
140	145	150
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 <213> Homo sapiens

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 ggcgtccttg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150
 tgcgctgcta cgtctgtccg gagccacag gagtgtcgga ctgtgtcacc 200
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
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 ccggtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
 tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
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<210> 454
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 454

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Cys	Gly	Glu	Leu	Ala	Pro	Ala	Leu	Arg	Cys	Tyr	Val	Cys	Pro	Glu
			20						25				30	
Pro	Thr	Gly	Val	Ser	Asp	Cys	Val	Thr	Ile	Ala	Thr	Cys	Thr	Thr
				35					40				45	
Asn	Glu	Thr	Met	Cys	Lys	Thr	Thr	Leu	Tyr	Ser	Arg	Glu	Ile	Val
				50					55				60	
Tyr	Pro	Phe	Gln	Gly	Asp	Ser	Thr	Val	Thr	Lys	Ser	Cys	Ala	Ser
				65					70				75	
Lys	Cys	Lys	Pro	Ser	Asp	Val	Asp	Gly	Ile	Gly	Gln	Thr	Leu	Pro
				80					85				90	
Val	Ser	Cys	Cys	Asn	Thr	Glu	Leu	Cys	Asn	Val	Asp	Gly	Ala	Pro
				95					100				105	
Ala	Leu	Asn	Ser	Leu	His	Cys	Gly	Ala	Leu	Thr	Leu	Leu	Pro	Leu
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<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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 <211> 266
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val
 50 55 60
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln
 65 70 75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
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Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
			95						100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
			110						115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
			125						130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
			140						145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
			155						160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
			170						175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
			185						190					195	
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			200						205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
			215						220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
			230						235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
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<213> Homo sapiens

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<223> unknown base

<400> 457

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<211> 4040

<212> DNA

<213> Homo sapiens

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 <212> PRT
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 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75
 Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu
 80 85 90
 Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu
 95 100 105
 Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr
 110 115 120
 Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu
 125 130 135
 Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe
 140 145 150
 Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala
 155 160 165
 Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg
 170 175 180
 Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met
 185 190 195
 Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly

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				215					220					225
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu
				230					235					240
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala
				245					250					255
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys
				260					265					270
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu
				275					280					285
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn
				290					295					300
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg
				305					310					315
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn
				320					325					330
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu
				335					340					345
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala
				350					355					360
Pro	Asp	Ile	Cys	Ser	Asn	Leu	Tyr	Val	Phe	Gln	Pro	Ser	Leu	Ala
				365					370					375
Val	Phe	Lys	Gly	Gln	Gly	Thr	Lys	Glu	Tyr	Glu	Ile	His	His	Gly
				380					385					390
Lys	Lys	Ile	Leu	Tyr	Asp	Ile	Leu	Ala	Phe	Ala	Lys	Glu	Ser	Val
				395					400					405
Asn	Ser	His	Val	Thr	Thr	Leu	Gly	Pro	Gln	Asn	Phe	Pro	Ala	Asn
				410					415					420
Asp	Lys	Glu	Pro	Trp	Leu	Val	Asp	Phe	Phe	Ala	Pro	Trp	Cys	Pro
				425					430					435
Pro	Cys	Arg	Ala	Leu	Leu	Pro	Glu	Leu	Arg	Arg	Ala	Ser	Asn	Leu
				440					445					450
Leu	Tyr	Gly	Gln	Leu	Lys	Phe	Gly	Thr	Leu	Asp	Cys	Thr	Val	His
				455					460					465
Glu	Gly	Leu	Cys	Asn	Met	Tyr	Asn	Ile	Gln	Ala	Tyr	Pro	Thr	Thr
				470					475					480
Val	Val	Phe	Asn	Gln	Ser	Asn	Ile	His	Glu	Tyr	Glu	Gly	His	His
				485					490					495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	500	505	510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	515	520	525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	530	535	540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	545	550	555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	560	565	570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	575	580	585
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Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	605	610	615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	620	625	630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	635	640	645
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	650	655	660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	665	670	675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	680	685	690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	695	700	705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	710	715	720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	725	730	735
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 461
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 461
 gatcagccag ccaataccag cagc 24

<210> 462
 <211> 50
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 462
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<210> 463
 <211> 1818
 <212> DNA
 <213> Homo sapiens

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<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

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Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg
 20 25 30

Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	155	160	165
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	170	175	180
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	185	190	195
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	200	205	210
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	215	220	225
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	230	235	240
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	245	250	255
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	260	265	270
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	275	280	285
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	290	295	300

<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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20 25 30

Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys
230 235 240

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
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 <211> 1071
 <212> DNA
 <213> Homo sapiens

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<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

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				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120

Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	125	130	135
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	140	145	150
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	155	160	165
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	170	175	180
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	185	190	195
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	200	205	210
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	215	220	225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	230	235	240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	245	250	255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser	260	265	270

<210> 469

<211> 687

<212> DNA

<213> Homo sapiens

<400> 469

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<210> 470
<211> 180
<212> PRT
<213> Homo sapiens

<400> 470
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Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
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Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 471
<211> 2368
<212> DNA
<213> Homo sapiens

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cgccccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45

Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75

Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	170	175	180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	185	190	195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	200	205	210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	215	220	225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	230	235	240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	245	250	255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	260	265	270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	275	280	285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	290	295	300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	305	310	315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	320	325	330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	335	340	345
Asp Lys Gly Leu																	

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 474
ctctcctcat ccacaccagc agcc 24

<210> 475
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476
<211> 2478
<212> DNA
<213> Homo sapiens

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caggggcaga aagaaaagag ctcccaaagt ctatatctat tcaggggctc 150
tcaagaacaa tggaatatca tctgatttta gaaaatttgg atgaagatgg 200
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250
tttcagagaa aggatcgtgt gctgcattct ctccttggcg cctcattgct 300
gtaatttttg gaatcctatg cttggtaata ctgggtgatag ctgtgggtcct 350
gggtaccatg ggggttcttt ccagcccttg tcctcctaata tggattatat 400
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2478

<210> 477
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477
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 20 25 30
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser

170

175

180

Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
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Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 478

gtccacagac agtcattctca ggagcag 27

<210> 479

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 479

acaagtgtct tcccaacctg 20

<210> 480

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 480

atcctcccag agccatggta cctc 24

<210> 481

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 481

ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50

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<210> 482

<211> 3819

<212> DNA

<213> Homo sapiens

<400> 482

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 aaaaaaaaaa aaaaaaaaaa 3819

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 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483
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 20 25 30
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	80	85	90
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr			

365	370	375
Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	
380	385	390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	
395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	
410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	
425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	
440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	
455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	
470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	
485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	
500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	
515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	
530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	
545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	
560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	
575	580	585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	
590	595	600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	
605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	
620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	
635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	
650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 68, 70, 84, 147
<223> unknown base

<400> 484
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cgggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
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tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
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tttctgttca acatgg 516

<210> 485
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 485
ggcattggag cagtgtggg tg 22

<210> 486
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 486

tggaggccta gatgcggctg gacg 24

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150

gcatctctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200

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cggagtacaa gacctcagc atgagagaat tattactgtg tctactaatg 450

gaagtattca cagcccaagg ttctctcata cttatccaag aaatacggctc 500

ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550

gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600

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tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700

aattaggata agatttgtat ctgatgaata ttttcttct gaaccagggt 750

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly	1	5	10	15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	20	25	30	
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180	
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr	185	190	195	

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	200	205	210
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	215	220	225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	230	235	240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	245	250	255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	260	265	270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	275	280	285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	290	295	300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	305	310	315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	320	325	330
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491
caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492
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<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 493
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<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494
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<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495
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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150
aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200
tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250
tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300
accattaacc acataccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400
gggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450
tttagtggac tcacttatctt aaaatccctt tacctggatg gaaaccagct 500
actagagata ccgcagggcc tccgcctag cttacagctt ctcagccttg 550
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aacatagaaa tactctacct gggccaaaac tgttattatc gaaatccttg 650
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acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu	
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Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	
				20					25					30	
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	
				35					40					45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	
				50					55					60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	
				65					70					75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	
				80					85					90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	
				95					100					105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	
				110					115					120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	
				125					130					135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	
				140					145					150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	
				155					160					165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	
				170					175					180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	
				185					190					195	
Glu	Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser	
				200					205					210	
Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	
				215					220					225	
Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	
				230					235					240	
Gln	Glu	Asp	Asp	Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp	
				245					250					255	

Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480
Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp			

545										550					555				
Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val					
				560					565					570					
Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile					
				575					580					585					
Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys					
				590					595					600					
Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr					
				605					610					615					
Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His					
				620					625					630					
Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	Leu					
				635					640					645					
Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn					
				650					655					660					
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro					
				665					670					675					
Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe					
				680					685					690					
Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp					
				695					700					705					
Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn					
				710					715					720					
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile					
				725					730					735					
Arg	Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg					
				740					745					750					
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr					
				755					760					765					
Ser	Phe	Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu					
				770					775					780					
His	His	Asn	Arg	Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val					
				785					790					795					
Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr					
				800					805					810					
Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val					
				815					820					825					
Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu					
				830					835					840					

Ile Leu Phe Ser	Leu Ser Ile Ser Val	Ser Leu Phe Leu Met	Val
845		850	855
Met Met Thr Ala	Ser His Leu Tyr Phe	Trp Asp Val Trp Tyr	Ile
860		865	870
Tyr His Phe Cys	Lys Ala Lys Ile Lys	Gly Tyr Gln Arg Leu	Ile
875		880	885
Ser Pro Asp Cys	Cys Tyr Asp Ala Phe	Ile Val Tyr Asp Thr	Lys
890		895	900
Asp Pro Ala Val	Thr Glu Trp Val Leu	Ala Glu Leu Val Ala	Lys
905		910	915
Leu Glu Asp Pro	Arg Glu Lys His Phe	Asn Leu Cys Leu Glu	Glu
920		925	930
Arg Asp Trp Leu	Pro Gly Gln Pro Val	Leu Glu Asn Leu Ser	Gln
935		940	945
Ser Ile Gln Leu	Ser Lys Lys Thr Val	Phe Val Met Thr Asp	Lys
950		955	960
Tyr Ala Lys Thr	Glu Asn Phe Lys Ile	Ala Phe Tyr Leu Ser	His
965		970	975
Gln Arg Leu Met	Asp Glu Lys Val Asp	Val Ile Ile Leu Ile	Phe
980		985	990
Leu Glu Lys Pro	Phe Gln Lys Ser Lys	Phe Leu Gln Leu Arg	Lys
995		1000	1005
Arg Leu Cys Gly	Ser Ser Val Leu Glu	Trp Pro Thr Asn Pro	Gln
1010		1015	1020
Ala His Pro Tyr	Phe Trp Gln Cys Leu	Lys Asn Ala Leu Ala	Thr
1025		1030	1035
Asp Asn His Val	Ala Tyr Ser Gln Val	Phe Lys Glu Thr Val	
1040		1045	

<210> 497

<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

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cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150

gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200

tgcagcaatc gtcgactaca ggaagttccc caaacgggtgg gcaaatatgt 250

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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
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Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
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Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
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Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
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Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
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Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
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Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
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Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
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Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
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Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
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Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210
Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
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Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240
Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly
				245					250					255
Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys
				260					265					270
Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn
				275					280					285
Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg
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Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val
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Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Val	Ser	Gly
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Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser
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Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	350	355	360
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Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	380	385	390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	395	400	405
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Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	425	430	435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	440	445	450
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Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	515	520	525
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	530	535	540
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	545	550	555
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	560	565	570
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	575	580	585
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	590	595	600
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	605	610	615
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	620	625	630
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Leu	Ser	Leu	Asn	Arg	Leu	Lys	His	Ile	Pro	Asn	Glu	Ala	Phe	Leu
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Asn	Leu	Pro	Ala	Ser	Leu	Thr	Glu	Leu	His	Ile	Asn	Asp	Asn	Met
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Leu	Lys	Phe	Phe	Asn	Trp	Thr	Leu	Leu	Gln	Gln	Phe	Pro	Arg	Leu
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Glu	Leu	Leu	Asp	Leu	Arg	Gly	Asn	Lys	Leu	Leu	Phe	Leu	Thr	Asp
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Ser	Leu	Ser	Asp	Phe	Thr	Ser	Ser	Leu	Arg	Thr	Leu	Leu	Leu	Ser
				710					715					720
His	Asn	Arg	Ile	Ser	His	Leu	Pro	Ser	Gly	Phe	Leu	Ser	Glu	Val
				725					730					735
Ser	Ser	Leu	Lys	His	Leu	Asp	Leu	Ser	Ser	Asn	Leu	Leu	Lys	Thr
				740					745					750
Ile	Asn	Lys	Ser	Ala	Leu	Glu	Thr	Lys	Thr	Thr	Thr	Lys	Leu	Ser
				755					760					765
Met	Leu	Glu	Leu	His	Gly	Asn	Pro	Phe	Glu	Cys	Thr	Cys	Asp	Ile
				770					775					780
Gly	Asp	Phe	Arg	Arg	Trp	Met	Asp	Glu	His	Leu	Asn	Val	Lys	Ile
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Pro	Arg	Leu	Val	Asp	Val	Ile	Cys	Ala	Ser	Pro	Gly	Asp	Gln	Arg
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Gly	Lys	Ser	Ile	Val	Ser	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp
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				830					835					840
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Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr
				860					865					870
Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser
				875					880					885
Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu
				890					895					900
Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu
				905					910					915
Cys	Leu	Glu	Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp
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Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	
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Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe	
			950							955				960	
Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile	
			965							970				975	
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu	
			980							985				990	
Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro	
			995							1000				1005	
Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn	
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Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val	
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<223> Synthetic oligonucleotide probe

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<211> 1738
<212> DNA
<213> Homo sapiens

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<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

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Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
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Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507

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cggggtgact gagcggaagg ccaggcaggg ccttcctcct cttcctcctc 1450

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<210> 508
<211> 273
<212> PRT
<213> Homo sapiens

<400> 508
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20 25 30
Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
35 40 45
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
50 55 60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
65 70 75
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
80 85 90
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
95 100 105
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
110 115 120
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
125 130 135
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln
140 145 150
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu
155 160 165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly
170 175 180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
185 190 195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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ctgaggcccc agcaagggct aggggtccatc tccagtccca ggacacagca 150

gcggccacca tggccacgcc tggggtccag cagcatcagc agccccagg 200

accggggagg cacaggtggc cccaccacc cggaggagca gctcctgccc 250

ctgtccgggg gatgactgat tctcctccgc caggccaccc agaggagaag 300

gccaccccg cctggaggcac aggccatgag gggctctcag gaggtgctgc 350

tgatgtggct tctgggtgtg gcagtgggag gcacagagca cgcctaccgg 400

cccggccgta ggggtgtgtg tgctccgggt caacggggacc ctgtctccga 450

gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500

accggggcctg cagcacctac cgaaccatct ataggaccgc ctaccgccgc 550

agccctgggc tggcccctgc caggcctcgc tacgcgtgct gcccgggtg 600

gaagaggacc agcgggcttc ctggggcctg tggagcagca atatgccagc 650

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 gtgggcccctc agctgagga aggtacgagc tccctgctgg agcctgggac 1450
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<210> 510
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 510
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 20 25 30
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val
 35 40 45
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg
 50 55 60
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg
 65 70 75
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro
 80 85 90
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala
 95 100 105
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro
 110 115 120
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln
 125 130 135
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

	140		145		150
Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu	155		160		165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys	260		265		270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

tgagcagca atatgccagc c 21

<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514
<211> 2690
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 2039-2065
<223> unknown base

<400> 514
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agttgggtct ccgtgtttca ggccggctcc cccttccctgg tctcccttct 200
cccgtctgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250
ggacttttga tgatgtttga cccagcggca ggaatagcag gcaacgtgat 300
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tgcgaaaacc 350
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ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450
atggccgcgt catgatggcc cggcaaaaagg gcattttcta cctgaccctt 500
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550
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tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800
acatgaaga tcttcgggcc tccccgggcc tcccattgca gcattctgtga 850
caactgtgtg gagcgcttcg accatcaactg cccctgggtg gggaattgtg 900
ttggaaagag gaactaccgc tactttctacc tcttcattct ttctctctcc 950
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atctttgaaa attggcttct tggagacatt gaaagaaact cctggaactg 1050
ttctagaagt cctcatttgc ttcttttacac tctgggtccg cgtgggactg 1100

actggatttc atactttcct cgtggctctc aaccagacaa ccaatgaaga 1150
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 atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg ccccttgccc 1250
 cccagtgtgc tggatcgaag gggatatttg ccactggagg aaagtggaag 1300
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 actcccgaag agatgccacc tccagagccc ccagagccac cacaggaggc 1450
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 ctgctgccct ctcggttaac tcacctaaag gcctcgccc acctctggct 2400
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<210> 515
<211> 364
<212> PRT
<213> Homo sapiens

<400> 515
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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met
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Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile
35 40 45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu
50 55 60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu
65 70 75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp
80 85 90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile
95 100 105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln
110 115 120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile
125 130 135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro
140 145 150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe
155 160 165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn
170 175 180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr
185 190 195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser
200 205 210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr
215 220 225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tgaattaggt attatagggg tgggtgggggtt gatttttntt cctggaggct 100
 tttggctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcactct ttntctctcc cncctcaca tctatgtctt cgccttcaac 250
 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517
caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518
gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519
agtgggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520
ctcacctgaa atctctcata gccc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521
cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150
aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250
aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300
gtgcactatt gacaaccggg tcaccgggtt ggcttggtta aaccgcagca 350
ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgcgtgggtc 400
cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450
tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500
caaagacctc tagggccac ctcattgtgc aagtatctcc caaaattgta 550
gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
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gcccaccca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250
caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300
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aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600

gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650

aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala
1 5 10 15

Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro
20 25 30

Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val
35 40 45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp
50 55 60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu
65 70 75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
80 85 90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val
95 100 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp
110 115 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
125 130 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly
140 145 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro
155 160 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val
170 175 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln
185 190 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro
200 205 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile
215 220 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524
 <211> 503
 <212> DNA
 <213> Homo sapiens

<400> 524
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 tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200
 acccgggtgg cctggctaaa ccgcagcacc atcctctatg ctgggaatga 250
 caagtgggtgc ctggatcctc gcgtggctct tctgagcaac acccaaacgc 300
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 acctgctcgg tgcagacaga caaccaccca aagacctcta ggtccacct 400
 cattgtgcaa gtatctccca aaattgtaga gatttcttca gatctctcca 450
 ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500
 gag 503

<210> 525
 <211> 2602
 <212> DNA
 <213> Homo sapiens

<400> 525
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gcggggcāgc tgccgggagc cctgaatcac cgcttgccc gactccacca 100
 tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150
 aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctgggtctt 200
 agcaggtgcc tctctactgc tggctgcact gcttctgggc tgccttggtg 250
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 cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550
 cttgcctaca ggtggagcgc attgaggagc tgggagccca gccactgaga 600
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<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

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Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp		110	115	120
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Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His	680	685	690
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Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly	710	715	720
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 <223> unknown base

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 24

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<213> Artificial Sequence

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 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr
 110 115 120
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val
 125 130 135
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu
 140 145 150
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu
 155 160 165
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe
 170 175 180
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln
 185 190 195
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro
 200 205 210
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile
 215 220 225
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

230	235	240
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245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile		
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val		
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys		
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Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr		
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys		
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<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

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Thr	Gln	Gln	Ala	Ala	Phe	His	Gln	Ile	Ala	Met	Glu	Pro	Phe	Glu
			20					25					30	

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

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335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln		
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Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys		
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro		
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser		
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn		
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala		
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu		
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr		
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln		
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu		
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His		
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Glu Glu Asp Ala Gly Val Glu Cys Ser Val		
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<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

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 20 25 30
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 35 40 45
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp
 50 55 60
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu
 65 70 75
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser
 80 85 90
 Phe Val Ile Pro Cys Asn Asn Gln
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<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

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<210> 618

<211> 750

<212> PRT

<213> Homo Sapien

<400> 618

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Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45

Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60

Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75

Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	
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Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
				110					115					120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	
				125					130					135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	
				140					145					150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	
				155					160					165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	
				170					175					180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	
				185					190					195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	
				200					205					210	
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	
				215					220					225	
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
				230					235					240	
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	
				245					250					255	
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	
				260					265					270	
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	
				275					280					285	
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	
				290					295					300	
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	
				305					310					315	
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	
				320					325					330	
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	
				335					340					345	
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	
				350					355					360	
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	
				365					370					375	
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	

380										385					390				
Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu					
				395					400					405					
Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser					
				410					415					420					
Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala					
				425					430					435					
Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile					
				440					445					450					
Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	Asp					
				455					460					465					
Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu					
				470					475					480					
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu					
				485					490					495					
Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro					
				500					505					510					
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe					
				515					520					525					
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn					
				530					535					540					
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val					
				545					550					555					
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe					
				560					565					570					
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe					
				575					580					585					
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr					
				590					595					600					
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser					
				605					610					615					
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp					
				620					625					630					
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys					
				635					640					645					
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val					
				650					655					660					
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe					
				665					670					675					

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 620
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 620
 gaacatcagc gctcccggtg attcc 25

<210> 621
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 622
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<400> 623
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<210> 624
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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide probe

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